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<p>(54) Title: NUCLEIC ACIDS ENCODING DYSTROPHIN-ASSOCIATED PROTEINS</p> <p>(57) Abstract</p> <p>The subject disclosure relates to substantially pure nucleic acid sequences encoding at least a portion of a dystrophin-associated protein. Deoxyribonucleic acid can be expressed in a DNA expression construct. Protein produced in this manner can be used for a variety of purposes including immunization to produce antibodies. Such DNA expression constructs, and the protein encoded by same, are useful in therapeutic methods to complement a genetic defect which results in muscular dystrophy.</p>		

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NUCLEIC ACIDS ENCODING DYSTROPHIN-ASSOCIATED PROTEINSBackground of the Invention

Muscular dystrophy refers to a group of genetically determined myopathies characterized by progressive atrophy or degeneration of increasing numbers of individual muscle cells. The structural changes observed histologically are essentially the same in the various types of muscular dystrophies. This may, perhaps, suggest a common etiology. However, the distribution of the affected muscles is quite distinctive. This, along with the mode of inheritance, forms the basis of the classification of these diseases. The muscular dystrophies are traditionally subdivided by the patterns of initial muscle involvement, which in turn correlates fairly well with the type of genetic transmission. The three major forms of muscular dystrophy are as follows:

- 1) Duchenne's Muscular Dystrophy which affects most skeletal muscle groups and is transmitted by an X-linked recessive gene;
- 2) Limb Girdle Muscular Dystrophy, affecting principally the pelvic and shoulder girdle muscles and is transmitted by an autosomal recessive gene;
- and 3) Facioscapulohumeral Muscular Dystrophy, involves the muscles of the face and shoulder girdle and is transmitted by an autosomal dominant gene.

Recently, the defective gene responsible for Duchenne's Muscular Dystrophy (DMD) has been located on the X-chromosome. The DMD gene encodes for a large molecular weight protein product, called dystrophin. This protein is localized to the sarcolemmal membrane of normal skeletal muscle, but is absent from the skeletal muscle of people with DMD, as well as dogs and mice with dystrophic muscle. A more benign form of this X-linked

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recessive disease is Becker's Muscular Dystrophy which is caused by an abnormal DMD gene which encodes an abnormal dystrophin protein. The exact function of dystrophin and the reasons why its absence or abnormal structure results
5 in necrosis of dystrophic muscle fibers has not been determined. However, the amino acid sequence of dystrophin suggests that it is a membrane cytoskeletal protein.

The present technology for initial detection and
10 diagnosis of Duchenne's or Becker's Muscular Dystrophy relies on the use of an immunological probe to identify the presence of dystrophin, the absence of dystrophin, or the abnormal molecular weight or content of dystrophin in human muscle biopsies. It is not uncommon for genetic
15 diseases to involve the loss or abnormal synthesis of more than one component or protein. In the case of muscular dystrophy, proteins other than dystrophin may be involved which are translated from genes located on different chromosomes (X chromosomes and/or autosomal
20 chromosomes), resulting in the different forms of muscular dystrophy. The identification of other potential proteins involved in muscular dystrophy and methods of quantifying these proteins would be immensely useful to clinicians for confirming diagnosis of
25 Duchenne's and Becker's muscular dystrophy, as well as, perhaps providing an initial diagnosis of other forms of muscular dystrophy. In addition, knowledge of the function of these proteins may lead to methods of predicting prognosis of disease progression and perhaps
30 therapeutic treatments for patients with muscular dystrophy in all of its various forms.

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Summary of the Invention

The present invention relates to substantially pure nucleic acid sequences encoding at least a portion of the core protein of a dystrophin-associated protein. The substantially pure nucleic acid sequence can be any nucleic acid sequence (i.e., DNA or RNA). The nucleic acid sequence can be isolated using a method similar to those described herein, or using another method. In addition, such nucleic acid can be synthesized chemically.

In a preferred embodiment, the substantially pure nucleic acid is characterized by the ability to hybridize to the nucleic acid sequence of SEQ ID NO: 1 under stringent hybridization conditions. One example of a set of conditions considered to be stringent is 50% formamide, 5 X SSPE (1 X SSPE is 0.15 M NaCl, 1 mM Na-EDTA, 10 mM Na-phosphate, pH 7.0), 5 X Denhardt's solution (0.1% polyvinylpyrrolidone, 0.1% Ficoll) at 45°C. The invention also relates to DNA expression vectors containing a substantially pure deoxyribonucleic acid sequence in expressible form, and cells transformed with same.

Both polyclonal and monoclonal antibodies can be prepared using, as the immunogen, proteins (or portions thereof) produced using such an expression vector. In addition, the nucleic acid sequence information can be used to design synthetic peptides for use as immunogen. Such antibodies can be used for a variety of purposes including affinity purification of dystrophin-associated proteins and diagnosis of autosomal muscular dystrophy. Also disclosed herein is the use of such antibodies in a non-invasive method for detecting muscular dystrophy.

The substantially pure nucleic acid can be used in gene therapy protocols to complement an autosomal-mutation based form of muscular dystrophy. The term

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"autosomal-mutation based" is used to distinguish forms of muscular dystrophy which result from mutations in the dystrophin gene which is X-linked (e.g., Duchenne and Becker muscular dystrophy).

5 Detailed Description of the Invention

Dystrophin is a large molecular weight protein product of the defective gene responsible for Duchenne's Muscular Dystrophy. This invention is based, in part, on the discovery that dystrophin exists as a component of a
10 large oligomeric complex in the sarcolemmal membrane of normal skeletal muscle. Proteins and glycoproteins comprise the other components of this complex which is referred to herein as the dystrophin-glycoprotein complex. Specifically, the other components comprise a
15 156 kDa glycoprotein, a 50 kDa glycoprotein, a 43 kDa glycoprotein, a 35 kDa glycoprotein, a 25 kDa protein and a triplet of proteins of 59 kDa molecular weight. These components are referred to as the non-dystrophin components of the dystrophin-glycoprotein complex.

20 Isolation of the Dystrophin-Glycoprotein Complex

The dystrophin-glycoprotein complex can be isolated from detergent solubilized skeletal muscle membranes using affinity chromatography and density gradient ultracentrifugation. Lectins are proteins or
25 glycoproteins which bind certain sugars or oligosaccharides. This property can be used to isolate certain glycoproteins from a complex mixture and is extremely useful as a general approach to the purification of membrane proteins, many of which are glyco-
30 sylated. In the present invention, the linked components

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of the dystrophin-glycoprotein complex can be isolated as an intact complex with lectins that bind to the glycoprotein components of the complex. The lectins are typically coupled to a solid support such as a

5 chromatographic gel (i.e., sepharose, agarose, etc.) and a complex mixture of membrane components is passed through a chromatography column containing the gel with bound lectin. The glycoproteins of membrane components bind to the lectin while the other components of the

10 mixture pass through the column. As described in greater detail below, a variety of lectins can be used in affinity-based methodologies to isolate the dystrophin-glycoprotein complex.

The dystrophin-glycoprotein complex can be further

15 purified using density gradient ultracentrifugation. The eluate from the affinity column as described above is applied as a narrow band to the top of a solution in a centrifuge tube. To stabilize the sedimenting components of the eluate against convection mixing, the solution

20 beneath the band contains an increasingly dense solution of an inert, highly soluble material such as sucrose (a density gradient). Under these conditions, the different fractions of the eluate sediment at different rates forming distinct bands that can be individually

25 collected. The rate at which each component sediments depends on its size and shape and is normally expressed as its sedimentation coefficient or S value.

Present day ultracentrifuges rotate at speeds up to about 80,000 rpm and produce forces up to about 500,000 x

30 gravity. At these enormous forces, even relatively small macromolecules, such as tRNA molecules and simple enzymes, separate from one another on the basis of their

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size. Using this technique, the size of the dystrophin-glycoprotein complex was estimated to be approximately 18S by comparing its migration to that of standards of varying size.

5 Another form of affinity chromatography which can be used to isolate the dystrophin-glycoprotein complex is known as immunoaffinity purification. This technique utilizes the unique high specificity of polyclonal and monoclonal antibodies as well as selected lectins. Such
10 highly specific molecules are extremely valuable tools for rapid, selective purification of antigens. In principle, the antigen is coupled (immobilized) on a column support and this is used to selectively adsorb antigen from a mixture containing many other antigens.
15 The antigens for which the antibody has no affinity can be washed away, and the purified antigen then eluted from the bound antibody or lectin with an elution buffer. Examples of antibodies and lectin molecules which are useful for the immunopurification of the dystrophin
20 complex components are described in detail below.

 The separation and isolation of the components of the dystrophin-glycoprotein complex can be accomplished by SDS-polyacrylamide gel electrophoresis (SDS-PAGE). In this technique, proteins are reacted with the detergent
25 sodium dodecylsulfate (SDS), to form negatively charged complexes. The amount of SDS bound by a protein, and consequently the charge on the complex, is roughly proportional to its size. Commonly, about 1.4 grams SDS is bound per 1 gram protein, although there are
30 exceptions to this rule. The proteins are generally denatured and solubilized by their binding of SDS, and the complex forms a prolate ellipsoid or rod of a length roughly proportionate to the molecular weight of the protein. Thus, proteins of either acidic or basic
35 isoelectric point form negatively charged complexes that

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can be separated on the basis of differences in charges and sizes by electrophoresis through a sieve-like matrix of polyacrylamide gel.

An alternative method for isolating the components of the dystrophin-glycoprotein complex is gel filtration high pressure liquid chromatography. This technique, in addition to taking less time than SDS gel electrophoresis, allows easier quantitation and recovery of separated proteins, and the resolution is better than that achieved by gel filtration with conventional materials.

Preparation of Antibodies Reactive with Components of the Dystrophin-Glycoprotein Complex

Monoclonal and polyclonal antibodies specific for non-dystrophin components of the dystrophin-glycoprotein complex are particularly useful in the isolation and diagnostic methods of this invention. Monoclonal antibodies useful in this invention are obtained by well known hybridoma methods. An animal is immunized with a preparation containing the dystrophin-glycoprotein complex. A fused cell hybrid is then formed between antibody-producing cells from the immunized animal and an immortalizing cell such as a myeloma.

In preferred embodiments, anti-non-dystrophin component monoclonal antibodies of this invention are produced by murine hybridomas formed by fusion of: a) mouse myeloma or hybridoma which does not secrete antibody with b) murine spleen cells which secrete antibodies obtained from mice immunized against dystrophin-glycoprotein complex.

Typically, the mice are immunized with a primary injection of dystrophin-glycoprotein complex followed by a number of boosting injections of dystrophin-glycoprotein complex. During or after the immunization

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procedure, sera of the mice may be screened to identify those mice in which a substantial immune response to the complex has been evoked. From selected mice, the spleen cells are obtained and fusions are performed. Suitable fusion techniques are the Sendai virus technique (Kohler, G. and Milstein, C., Nature, 256: 495 (1975)), or the polyethylene glycol method (Kennet, R.H., "Monoclonal Antibodies, Hybridomas--A New Dimension in Biological Analysis," Eds. R.H. Kennet, T.J. McKern and K.B. Bechtol, Plenum Press, NY (1980)).

The hybridomas are then screened for production of anti-non-dystrophin component antibodies. A suitable screening technique is a solid phase radioimmunoassay. A solid phase immunoabsorbent is prepared by coupling dystrophin-glycoprotein complex or non-dystrophin components to an insoluble matrix. The immunoabsorbent is brought into contact with culture supernatants of hybridomas. After a period of incubation, the solid phase is separated from the supernatants, then contacted with a labeled antibody against murine immunoglobulin. Label associated with the immunoabsorbent indicates the presence of hybridoma products reactive with dystrophin-glycoprotein complexes or non-dystrophin components. The hybridoma products are then examined for their ability to react with natural and synthetic components of the dystrophin-glycoprotein complex.

The monoclonal anti-non-dystrophin component antibodies can be produced in large quantities by injecting anti-non-dystrophin component antibody producing hybridoma cells into the peritoneal cavity of mice and, after an appropriate time, harvesting ascites fluid from the mice which yield a high titer of homogenous antibody. The monoclonal antibodies are isolated therefrom. Alternatively, the antibodies can be produced by culturing anti-non-dystrophin component antibody

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producing cells in vitro and isolating secreted monoclonal anti-non-dystrophin component antibodies from the cell culture medium directly.

Another method of forming antibody-producing cells is by viral or oncogenic transformation. For example, a B-lymphocyte which produced a non-dystrophin component specific antibody may be infected and transformed with a virus, such as the Epstein-Barr virus, to give an immortal antibody-producing cell (Kozbon and Roder, Immunol. Today 4: 72-79 (1983)). Alternatively, the B-lymphocyte may be transformed by a transforming gene or gene product.

Polyclonal antibodies can be prepared by immunizing an animal with a crude preparation of the dystrophin-glycoprotein complex or the purified non-dystrophin components of the complex. The animal is maintained under conditions whereby antibodies reactive with the components of the complex are produced. Blood is collected from the animal upon reaching a desired titer of antibodies. The serum containing the polyclonal antibodies (antisera) is separated from the other blood components. The polyclonal antibody-containing serum can optionally be further separated into fractions of particular types of antibodies (e.g., IgG or IgM) or monospecific antibodies can be purified from polyclonal antibody containing serum.

Diagnostic Methods

An observation which is fundamental to the subject invention is that there is a strong correlation between the absence or reduction in the quantity of the non-dystrophin components of the dystrophin-glycoprotein complex and affliction by muscular dystrophy. As described in the Exemplification below, monoclonal or polyclonal antibodies can be used to detect the absence

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or reduction of a particular non-dystrophin component of the complex. In both mouse and human samples of dystrophic tissue, muscular dystrophy can be diagnosed by detecting reduction or absence of non-dystrophin components of the complex. This analysis can be extended beyond the Duchenne-type muscular dystrophy (X-linked) to the detection of autosomal-based muscular dystrophy as demonstrated in the Exemplification in connection with Fukuyama congenital muscular dystrophy.

10 In one embodiment of the diagnostic method of the invention, a muscle biopsy sample is treated in a procedure which renders the non-dystrophin components available for complexing with antibodies directed against said components. Muscle samples are obtained from patients by surgical biopsy. The site of biopsy could be any skeletal muscle suspected of being dystrophic. Muscle groups about the shoulder and pelvic girdles, however, are the most affected, and are likely to be the most common site of biopsy. The amount of muscle
20 obtained should be enough to extract the components of the dystrophin-glycoprotein complex from muscle membranes and detect their presence by the diagnostic methods described within this application. Alternative methods of extraction can be used.

25 For biopsy samples greater than 500 mg, the muscle tissue can be homogenized by mechanical disruption using apparatus such as a hand operated or motor driven glass homogenizer, a Waring blade blender homogenizer, or an ultrasonic probe. Homogenization can occur in a buffer comprising 20 mM sodium pyrophosphate, 20 mM sodium
30 phosphate monohydrate, 1 mM magnesium chloride, 0.303 M sucrose, 0.5 mM EDTA, pH 7.1, with various protease inhibitors such as aprotinin (0.5 µg/ml), benzamidine (100 µg/ml), iodoacetamide (185 µg/ml), leupeptin (0.5
35 µg/ml), pepstatin A (0.5 µg/ml) and PMSF (40 µg/ml).

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Heavy microsomes can be prepared from homogenized skeletal muscle by the method of Mitchel, et al. (J. Cell. Biol., 95: 1008-1016 (1983)). The microsomes are then washed with a physiological salt solution and
5 solubilized in saline containing detergent and protease inhibitors. Following solubilization of the microsomes, the sample is treated with SDS. In the present case, SDS acts to dissociate the linked components of the dystrophin-glycoprotein complex, thereby allowing their
10 separation.

For muscle biopsy samples less than 500 mg, an alternative extraction procedure can be used. Samples are frozen in liquid nitrogen and crushed using a mortar and pestle and prepared for electrophoresis by treatment
15 with SDS as described by Hoffman et al. (N. Eng. J. Med. 318: 1363-1368 (1988)), hereby incorporated by reference.

The components of the SDS treated sample are then separated electrophoretically. Following electrophoretic separation, the components of the dystrophin-glycoprotein
20 complex are transferred from the gel matrix to a solid support. The components are transferred out of the gel and onto a filter or membrane, forming an exact replica of the original protein separation, but leaving the transferred proteins accessible for further study. The
25 detection of transferred proteins can be accomplished by the use of general protein dyes such as Amido black or Coomassie brilliant blue. Alternatively, antibodies which are specific for the known non-dystrophin components of the dystrophin-glycoprotein complex can be
30 labeled with a detectable reporter group and used to bind to the various components. An example of this method is the well known Western blot method.

Alternatively, tissue specimens (e.g., human biopsy samples) can be tested for the presence of the components
35 of the dystrophin-glycoprotein complex by using mono-

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clonal or polyclonal antibodies in an immunohistochemical technique, such as the immunoperoxidase staining procedure. In addition, immunofluorescent techniques can be used to examine human tissue specimens. In a typical
5 protocol, slides containing cryostat sections of frozen, unfixed tissue biopsy samples are air-dried and then incubated with the anti-non-dystrophin component antibody preparation in a humidified chamber at room temperature. The slides are layered with a preparation of
10 fluorescently labeled antibody directed against the monoclonal antibody. The staining pattern and intensities within the sample are determined by fluorescent light microscopy.

The antibodies of the present invention can also be
15 used in an enzyme-linked immunoadsorbant assay (ELISA) for determining the absence or presence of non-dystrophin components of the dystrophin-glycoprotein complex. Antibodies against non-dystrophin components to be measured are adsorbed to a solid support, in most cases a
20 polystyrene microtiter plate. After coating the support with antibody and washing, a solubilized sample is added. If a non-dystrophin component is present for which the antibodies are specific, they will bind to the adsorbed antibodies. Next, a conjugate that will also bind to the
25 non-dystrophin component is added. Conjugates are secondary antibody molecules to which an enzyme is covalently bound. After addition of a chromogenic substrate for the enzyme, the intensity of the colored reaction products generated will be proportional to the
30 amount of conjugated enzyme and thus indirectly to the amount of bound non-dystrophin component. Since the intensity of the developed color is proportional to the amount of non-dystrophin component present, determination of the intensity of the color produced by a standard
35 series of non-dystrophin component concentrations will

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allow the calculation of the amount of non-dystrophin component in an unknown sample. Many variations of this assay exist as described in Voller, A., Bidwell, D.E. and Bartlett, A., The Enzyme Linked Immunoabsorbent Assay (ELISA): A guide with abstracts of microplate applications, Dynatech Laboratories, Alexandria, Virginia (1979) and are hereby incorporated by reference.

In another embodiment of the diagnostic method, antibodies specifically reactive with an extracellular component of the dystrophin-glycoprotein complex (e.g., the 156 kDa component) are labeled with a detectable reporter group and administered (e.g., intravenously) to an individual to be tested for muscular dystrophy using conventional immunodiagnostic methods. The extracellular components of the dystrophin-glycoprotein complex are exposed on the surface of an intact cell and therefore, are reactive with labeled circulating antibodies which have the ability to pass through capillary membranes to reach the muscle tissue surface. Thus, the disruption of the cell is not necessary for diagnosis.

Isolation of Nucleic Acids Encoding Dystrophin-Associated Proteins and Uses for Same

Antibodies reactive with dystrophin-associated proteins can be used to isolate and purify nucleic acid which encodes the proteins. This can be accomplished in a variety of ways. For example, monospecific polyclonal antibodies, or monoclonal antibodies, can be used in affinity purification methods to isolate highly purified preparations of individual dystrophin-associated glycoproteins (DAGs). Using standard biochemical techniques (e.g., Edman degradation), the amino acid sequence of a portion of the protein can be determined. Using this protein sequence information, degenerative nucleic acid probes can be designed and synthesized.

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Such probes can be used to screen nucleic acid libraries (e.g., cDNA libraries from tissues known to express the dystrophin-associated proteins). DNA sequences identified by such a screening method can be used to
5 isolate overlapping clones. This process leads ultimately to the reconstruction of the entire coding region.

Alternatively, monoclonal or polyclonal antibodies can be used to screen an expression library, such as a
10 genomic DNA library prepared in the vector λ gt11. The λ gt11 system enables the expression of DNA fragments from a DNA library of interest (e.g., a human genomic DNA library) as a beta-galactosidase fusion protein. Recombinant phage are plated on a lawn of bacteria and
15 the recombinants are screened immunologically using conventional techniques.

Once isolated, the DNA encoding components of the dystrophin-associated proteins can be used in a variety of ways. For example, the DNA can be inserted in an
20 expression vector. Such vectors contain all necessary regulatory signals to promote the expression of a DNA segment of interest. Expression vectors are typically either prokaryote specific, or eukaryote specific. However, vectors have been developed which can promote
25 the expression of a DNA sequence of interest in either a prokaryotic or eukaryotic system. Such vectors are known as shuttle vectors.

Prokaryotic expression vectors are useful for the preparation of large quantities (up to milligram
30 quantities) of the protein encoded by a DNA sequence of interest. This protein, or immunogenic peptide portions of same, can be used for example, as a source of highly pure immunogen for the generation of antibodies specific to components of the complex. Immunogenic peptides can
35 also be produced synthetically from the known DNA

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sequence. Alternatively, as discussed in detail below, some proteins may be useful for therapeutic applications.

As has been discussed previously, several of the dystrophin-associated proteins are extensively glycosylated. Because prokaryotic systems do not possess the cellular machinery necessary to reproduce this glycosylation, it may be desirable to produce the proteins in a eukaryotic system using a eukaryotic expression system.

While Duchenne and Becker muscular dystrophy are characterized by the absence, or reduction in the abundance of, dystrophin (as well as the dystrophin-associated proteins) in afflicted individuals, this is not true with all forms of muscular dystrophy. It has been observed, for example, that an autosomal mutation-based muscular dystrophy is characterized by near normal levels of dystrophin, but substantially reduced levels of the dystrophin-associated proteins. For example, in patients suffering from Fukuyama congenital muscular dystrophy (FCMD), all of the dystrophin-associated glycoproteins were found to be substantially diminished whereas the abundance of dystrophin was only mildly reduced when compared to control samples. It is highly likely that many of the autosomal mutation-based muscular dystrophies result from deleterious mutations in the genes encoding one or more of the dystrophin-associated proteins. Thus, one use for a DNA expression vector encoding a dystrophin-associated protein would be to complement such a mutation.

The DNA expression vector can be introduced into the individual in a variety of ways. For example, myoblast cells can be isolated from the afflicted individual by biopsy, transformed with the expression construct in vitro and reintroduced to the afflicted individual by intramuscular injection. Alternatively, the DNA

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expression construct can be administered directly to the afflicted individual, for example, by intramuscular injection.

5 In addition to the use of expression vectors to mediate gene therapy, the administration dystrophin-associated protein, or portions thereof, to an afflicted individual may also offer a viable therapeutic alternative. Because of the difficulties associated with introducing a protein into a cell across the cell
10 membrane, this therapeutic approach is would be most useful for muscular dystrophies characterized by the absence or reduction in abundance of an extracellular protein. The 156 kDa dystrophin-associated protein is such a protein.

15 In addition, the 156 kDa dystrophin-associated protein is characterized by other properties which suggest that this type of therapy would be effective. For example, as reported in the Exemplification section which follows, the 156 kDa protein binds laminin which is
20 one of the major components of the extracellular matrix. In fact, it appears to be a high affinity laminin binding protein. Although the mechanism underlying the fact that dystrophin deficiency causes the muscle cell necrosis characteristic of muscular dystrophy is unknown,
25 experiments suggest that dystrophin functions to link the subsarcolemmal membrane cytoskeleton through a transmembrane complex to an extracellular glycoprotein which binds laminin. Although the exact function of the 156 kDa protein is not known, muscle cells do interact
30 with the extracellular matrix via specific cell surface receptors and thus it is likely that the 156 kDa protein is involved in the interactions between sarcolemma and extracellular matrix.

In a therapeutic method, the 156 kDa protein, or a
35 laminin binding domain thereof, would be administered

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(preferably intravenously) to an afflicted individual.

At the surface of the muscles tissue, the 156 kDa protein, or the laminin binding portion thereof, is expected to interact with the sarcolemma and

5 extracellular matrix thereby stabilizing the tissue. The progress of therapy can be monitored, for example, by a combination of muscle strength measurement and muscle biopsy analysis.

The DNA sequence information can also be used in
10 diagnostic applications. As discussed above, many of the autosomal mutation-based muscular dystrophies are likely to result from mutations in the DNA encoding a dystrophin-associated protein. Thus, one method for diagnosing autosomal muscular dystrophy involves
15 identifying mutations in the DNA sequence encoding a dystrophin-associated protein which correlates with the disease phenotype. This can be done, for example, using immunohistochemical techniques as described in the Examples which follow. DNA encoding a dystrophin-
20 associated protein can be isolated from an individual whose affliction has been demonstrated in such a manner. The DNA sequence of the gene from an afflicted individual can be compared with the DNA sequence of the gene from a non-afflicted individual. Using this technique,
25 particular mutations are identified which correlate with the disease phenotype. Using this information, synthetic oligonucleotide probes can be synthesized which facilitate the rapid detection of such mutations in a DNA sample from an individual to be tested for autosomal
30 muscular dystrophy.

For example, if the mutation which correlates with the disease phenotype is found to be a point mutation in the gene encoding the 156 kDa dystrophin-associated protein, a synthetic peptide of about 10-15 base pairs in
35 length can be synthesized. The sequence of the synthetic

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peptide should have a sequence which is perfectly complementary to the appropriate region of either the normal gene or the mutant gene. Using conventional hybridization techniques it is possible to rapidly
5 identify the presence of either the normal sequence or the mutant sequence in a sample of DNA from an individual to be tested.

The invention is now further and specifically illustrated by the following examples.

10

EXEMPLIFICATION

Example 1: Isolation and Characterization of Dystrophin-Glycoprotein Complex

Isolation of complex by density centrifugation

Heavy microsomes were prepared from rabbit skeletal
15 muscle by the method described in Mitchell, et al. (J. Cell. Biol. 95: 1008-1016 (1983)). The microsomes were washed twice with 0.6 M KCl in 50 mM tris-HCl, pH 7.4, 0.165 M sucrose, 0.1 mM PMSF and 0.75 mM benzamidine to remove contractile proteins. One gram of KCl-washed
20 membranes were solubilized in 1.0% digitonin, 0.5 M NaCl, and protease inhibitors as previously described in Campbell, K.P. and Kahl, S.D., Nature, 338: 259-262 (1989). After removal of the ryanodine receptor by immunoaffinity chromatography as described in Imagawa et
25 al. (J. of Biol. Chem., 262: 16636-16643 (1987)), the digitonin-solubilized membranes were circulated overnight in a 40 ml WGA sepharose column, washed extensively, then eluted with three column volumes of 0.3 M N-acetyl-glucosamine.

30

Eluted fractions containing dystrophin were applied to a 3 ml DEAE cellulose column and sequentially eluted with the following NaCl concentrations in buffer A (0.1%

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digitonin, 50 mM tris-HCl, pH 7.4, 0.75 mM benzemidine, 0.1 mM PMSF): 0 mM, 25 mM, 50 mM, 75 mM, 100 mM, 110 mM and 175 mM. Sucrose gradients (12.5 ml linear 5% to 20% sucrose) containing 0.5 M NaCl and 0.01% NaN_3 in buffer A were prepared using a Beckman density gradient former. Dystrophin-glycoprotein complex, which eluted in fraction two (3 ml) from the DEAE-column 175 mM NaCl wash was concentrated to 0.5 ml in a centricon-100 (Amicon), layered on a sucrose gradient, and overlaid with 0.5 ml of buffer A containing 175 mM NaCl and 0.01% NaN_3 . Gradients were centrifuged at 4°C in a Beckman VTi 65.1 vertical rotor for 90 minutes at 200,000XG. Fractions (0.6 ml) were collected from the top of the gradients using an ISCO Model 640 density gradient fractionator.

15 Affinity characterization of dystrophin-glycoprotein complex

Gradient fractions were separated by SDS-PAGE (3% to 12% gradient gel) and stained with Coomassie Blue (300 ul of fractions concentrated to 50 ul with a centricon-100) or transferred to nitrocellulose and stained with various antibodies. Gel lanes were scanned with a Hoefer GS300 scanning densitometer and analyzed using GS-360 data analysis software.

Polyclonal antisera against a chemically synthesized decapeptide representing the C-terminal of dystrophin was raised in New Zealand white rabbits as previously described in Strynadka, N.C.J., et al., J. of Virol., 62: 3474-3483 (1988). Hybridomas were obtained from female balb/C mice which were immunized with rabbit skeletal muscle membranes and boosted with WGA eluate as described in Jorgensen, A.O., et al., Cell Motility and Cytoskeleton, 9: 164-174 (1988).

It was evident from the Coomassie Blue-stained gel of sequential gradient fractions that the dystrophin-

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glycoprotein complex was clearly separated from the voltage-sensitive sodium channel and the dihydropyridine receptor. The size of the dystrophin-glycoprotein complex was estimated to be approximately 18 S by
5 comparing its migration to that of the standards B-galactosidase (15.9 S), thyroglobulin (19.2 S) and the dihydropyridine receptor (20 S). Densitometric scanning of the peak dystrophin-glycoprotein containing gradient fractions revealed several proteins which copurified with
10 dystrophin: a broad, diffusely staining component with an apparent M_r of 156 kDa, 88 kDa protein, a triplet of proteins centered at 59 kDa, 50 kDa protein, a protein doublet at 43 kDa, 35 kDa protein and a 25 kDa protein.

In order to identify the glycoprotein constituents
15 of the dystrophin-glycoprotein complex, sucrose gradient fractions were electrophoretically separated, transferred to nitrocellulose, and stained with peroxidase-conjugated WGA. Four WGA-binding proteins with apparent M_r of 156 k, 50 k, 43 k and 35 k were found to strictly copurify
20 with dystrophin. All four of the WGA-binding proteins were also stained with peroxidase-conjugated concanavalin A. In addition, the lower M_r component of the 43 kDa protein doublet, apparent with Coomassie Blue staining was also stained with concanavalin A. The
25 dystrophin-glycoprotein complex was further characterized with antibodies raised against various components of the complex. Antisera from a rabbit which was immunized with a chemically synthesized decapeptide representing the predicted C-terminal amino acid sequence of human
30 dystrophin was found to stain a single M_r protein. This protein comigrated with the predominant isoform of dystrophin stained by sheep polyclonal anti-dystrophin antibodies.

A library of monoclonal antibodies against muscle
35 proteins eluted from WGA-sepharose was also screened for

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reactivity against components of the dystrophin- glyco-
protein complex. Of six hybridomas which showed immuno-
fluorescence staining only on the sarcolemma monoclonal
antibodies XIXC2 and VIA4₂ were found to stain dystrophin
5 on immunoblots. Both dystrophin monoclonal antibodies
are IgM subtypes, and recognized both native and
denatured dystrophin. Monoclonal antibody XIXC2 also
recognized the minor lower M_r isoform of dystrophin which
appears to copurify with the more abundant isoform.

10 Two of the other sarcolemma-specific monoclonal
antibodies were specific for components of the
dystrophin-glycoprotein complex. The 50 kDa glycoprotein
stained with monoclonal antibody IVD3₁. Monoclonal IVD3₁
recognized only the nonreduced form of the 50 kDa glyco-
15 protein and it is not highly crossreactive. Monoclonal
antibody VIA4₁ stained the 156 kDa glycoprotein which
copurified with dystrophin. Monoclonal antibody VIA4₁
recognized the denatured form of the 156 kDa glycoprotein
and is highly crossreactive.

20 Immunolocalization of components of the dystrophin-
glycoprotein complex in rabbit muscle

The indirect immunofluorescence labeling of fixed 8
μm transverse cryostat sections from rabbit gastronimious
was carried out as described in Jorgensen, A.O., et al.,
25 supra. Sections were preincubated for 20 minutes with 5%
normal goat antiserum in phosphate buffered saline,
followed by a two hour incubation at 37°C with the
primary antibody (hybridoma supernatants or 1:1000
diluted antiserum). After washing in PBS, the sections
30 were further incubated for 30 minutes at 37°C in PBS with
a 1:50 dilution of FITC-labeled goat F(ab')₂ anti-mouse
IgG or anti-rabbit IgG and subsequently examined in a
Leitz fluorescence microscope. Staining of cryostat
sections was not observed with non-immunue serum, nor was

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there any nonspecific binding to the tissue by fluorescein-labeled secondary antibody.

The antisera to the C-terminal amino acid sequence of human dystrophin showed immunofluorescence staining only on the cell periphery which indicates a restricted localization of dystrophin to the sarcolemma of rabbit skeletal muscle. This observation was confirmed by staining rabbit skeletal muscle with monoclonal antibody XIXC2 against dystrophin and, again, localization was observed in the sarcolemma of the rabbit skeletal muscle. The 50 kDa glycoprotein, stained with monoclonal IVD3₁, has been localized exclusively to the sarcolemmal membrane of rabbit skeletal muscle. Monoclonal antibody VIA4₁ exhibited weak, but specific, immunofluorescent staining of the sarcolemmal membrane consistent with its low affinity for the native 156 kDa glycoprotein. In agreement with immunofluorescence results, a rabbit membrane preparation greatly enriched in sarcolemmal proteins also exhibits a substantial enrichment in dystrophin, the 156 kDa and 50 kDa glycoproteins. Immunofluorescence staining for dystrophin, 50 kDa glycoprotein or the 156 kDa glycoprotein was equally distributed in fast and slow muscle fibers.

Immunoabsorption of the dystrophin-glycoprotein complex

Immunoaffinity beads prepared as described in Campbell, K.P., et al., J. of Biol. Chem., 262: 6460-6463 (1987), were equilibrated with buffer A containing 0.5 M NaCl and then incubated overnight (12 hours) with 0.75 ml of fraction 2 from the 1.75 mM NaCl wash of the DEAE-cellulose column as described above. After pelleting, the supernatants were decanted (voids) and the affinity beads were washed with 5 x 0.7 ml aliquots of buffer A containing 0.5 M NaCl. The void from each affinity column and the five washes were pooled and concentrated

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to 375 ul in a centricon 100 (Amicon). In addition, 0.75 ml of fraction 2 was diluted to 4.2 ml with buffer A, concentrated to 375 ul and used as control. Column voids were analyzed by SDS-PAGE and immunoblotted as described above.

The voids from the XIXC2 (anti-dystrophin) and the IVD3₁ (anti-50 kDa glycoprotein) immunoaffinity beads contained no dystrophin, 59 kDa triplet, 50 kDa glycoprotein, 43 kDa doublet or 35 kDa proteins as detected by Coomassie Blue staining. It was apparent that both the XIXC2 (anti-dystrophin) and IVD3₁ (anti-50 kDa glycoprotein) immunoaffinity beads quantitatively removed dystrophin from the starting material. Analysis of the voids for the 156 kDa glycoprotein and the 50 kDa glycoprotein revealed that both the XIXC2 and the IVD3₁ immunoaffinity beads selectively adsorbed all but a trace of each of these glycoproteins from the voids while the voltage-sensitive sodium channel, and the alpha₁ and alpha₂ subunits of the dihydropyridine receptor remained in the voids. As detected by peroxidase-conjugated WGA, the 43 kDa and 35 kDa glycoproteins were also adsorbed from the voids. Immunoblots of immunoaffinity beads separated on gels indicated that dystrophin, the 156 kDa and 50 kDa glycoproteins were retained by the beads and not selectively proteolyzed. Initial experiments with monoclonal VIA4₁ (anti-156 kDa glycoprotein) have indicated that it has too low an affinity for the native 156 kDa glycoprotein to be successful in this type of an experiment.

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Example 2: Reduction or Absence of 156 kDa
 Glycoprotein in Dystrophic Mammals

Immunoblot analysis of control and dystrophic mouse
muscle membranes

5 Membranes from control and dystrophic mice (mdx)
were prepared in 10% sucrose, 76.8 mM aprotinin, 0.83 mM
benzamidine, 1 mM iodoacetamide, 1.1 uM leupeptin, 0.7 uM
pepstatin A, 0.23 mM PMSF, 20 mM tris-maleate, pH 7.0, by
centrifuging muscle homogenates for 15 minutes for 14,000
10 XG and subsequently pelleting the supernatant for 30
minutes at 125,000 xg followed by KCl washing as
described above. Control and dystrophic mouse muscle
membranes were analyzed by SDS-PAGE and immunoblotting as
described above. The amount of 156 kDa glycoprotein in
15 each preparation was estimated densitometrically from
autoradiographs of identical blots incubated with ¹²⁵I-
labeled sheep anti-mouse secondary antibody.

 Staining with polyclonal antisera against the C-
terminal decapeptide of dystrophin revealed that
20 dystrophin was completely absent from dystrophic mouse
membranes. In addition, comparison of normal and
dystrophic mouse with immunostaining by monoclonal
antibody VIA4₁ against the 156 kDa glycoprotein revealed
that the 156 kDa glycoprotein was absent or greatly
25 reduced in dystrophic mouse membranes. Staining of
identical transfers with sheep polyclonal antisera
against either the ryanodine receptor, or the dihydro-
pyridine receptor, did not differ between control and
dystrophic mouse muscle membranes. Monoclonal antibody
30 IVD3₁ against the 50 kDa glycoprotein did not crossreact
with normal mouse membranes and, thus, could not be
evaluated. The absence of the 156 kDa glycoprotein was
also confirmed using SDS muscle extracts instead of
isolated membranes from control and dystrophic mice.

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Estimation of the 156 kDa glycoprotein remaining in the dystrophic muscle membranes using ^{125}I -labeled secondary antibodies and total membrane preparations from four different control and four different dystrophic mice revealed an average reduction of 85% in dystrophic muscle.

Immunoblot analysis of normal and dystrophic human muscle biopsies

Frozen muscle biopsy samples (50 mg) were crushed in liquid nitrogen using a mortar and a pestle and then prepared for electrophoresis as described by Hoffman, *et al.*, *N. Eng. J. of Med.*, 318: 1363-1368 (1988). The pulverized muscle samples were transferred to ten volumes of SDS-PAGE sample buffer (10% SDS, 2 M sucrose, 4% 2-mercaptoethanol, 0.002% bromophenyl blue, 260 mM tris-HCl, pH 6.8), vortexed, and precipitated material allowed to settle. Aliquots (50 μl) of the SDS-extracted muscle samples were analyzed by SDS-PAGE and immunoblotting and the amount of 156 kDa glycoprotein was estimated.

The dystrophic samples exhibited no staining with antibodies against dystrophin by indirect immunofluorescence microscopy and immunoblotting. In contrast to the normal muscle extract, the 3 DMD samples showed greatly reduced staining for the 156 kDa glycoprotein. On the other hand, identical immunoblots stained with monoclonal antibodies against the Ca^{2+} - dependent ATPase revealed no difference in the staining intensity between normal and dystrophic muscle samples. Again, the amount of 156 kDa glycoprotein was estimated to be reduced by approximately 90% in DMD samples.

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Example 3: Characterization of Dystrophin-Glyco-
protein Complex with Guinea Pig Antisera

Polyclonal antisera reactive with dystrophin-glycoprotein
complex

5 Polyclonal antisera specific for various components
of the dystrophin-glycoprotein complex were prepared by
two methods. In the first method, (see Sharp, A.H. and
Campbell, K.P., J. Biol. Chem. 266:9161-9165 (1989)),
individual components of the dystrophin-glycoprotein
10 complex (~500 μ g) were separated by SDS-PAGE in the
presence of 1% 2-mercaptoethanol. The gels were stained
for 10 min with Coomassie Blue in 10% acetic acid, 25%
isopropanol and destained in distilled water. Individual
bands were cut from the gel and frozen in 1 ml of PBS
15 until being used for immunization of guinea pigs.
Alternatively, 50 μ g of dystrophin-glycoprotein complex
in buffer A (0.1% digitonin, 50 mM Tris-HCl, pH 7.4, 0.75
mM benzamidine, 0.1 mM PMSF) was used as immunogen.
Animals were boosted on day 14 with 5 μ g of the
20 appropriate antigen and monthly thereafter. Antisera
were collected weekly after sufficient titers had been
achieved. Antisera specific for each component of the
dystrophin-glycoprotein complex were affinity-purified
using Immobilon-P transfers of individual proteins
25 separated by SDS-PAGE.

Antisera from guinea pigs immunized with purified
dystrophin-glycoprotein complex as described by Ervasti
et al. (J. Biol. Chem. 266:9161-9165 (1991)), showed
immunoreactivity to all components of the complex with
30 the exception of the 50 kDa dystrophin-associated
glycoprotein. Immobilon-P transfer strips containing
individual components of the dystrophin-glycoprotein
complex separated by SDS-polyacrylamide gel
electrophoresis were used to affinity purify antibodies

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specific of the 156 kDa, 59 kDa, 43 kDa and 35 kDa dystrophin-associated proteins. Antibodies to the 50 kDa dystrophin-associated glycoprotein were affinity-purified from antisera obtained by immunizing a guinea pig with SDS polyacrylamide gel slices containing the reduced 50 kDa dystrophin-associated glycoprotein. Immunoblot staining of skeletal muscle microsomes, sarcolemma and purified dystrophin-glycoprotein complex demonstrated that each of the affinity-purified antibodies recognized only proteins of the same molecular weight to which they were raised an affinity purified against. This data suggests that the 156 kDa, 59 kDa, 50 kDa, 43 kDa and 35 kDa dystrophin-associated proteins are not proteolytic fragments of larger proteins or dystrophin.

15 Stoichiometric relationship between complex components

Densitometric analysis of Coomassie Blue-stained SDS-polyacrylamide gels containing the electrophoretically separated components of six different preparations of dystrophin-glycoprotein complex demonstrated that the 59 kDa, 50 kDa, 43 kDa, 35 kDa and 25 kDa dystrophin-associated proteins exhibited average stoichiometric ratios of 1.6 ± 0.22 , 0.82 ± 0.11 , 0.95 ± 0.14 , 1.8 ± 0.19 and 0.36 ± 0.12 relative to dystrophin. However, the stoichiometry of the 156 kDa dystrophin-associated glycoprotein relative to dystrophin has not been determined because it stains poorly with Coomassie Blue. Therefore, the antibody staining intensity was quantitated from autoradiograms of the immunoblots after incubation with [125 I]-Protein A and was compared to the Coomassie Blue staining intensity of dystrophin in sarcolemma and purified dystrophin-glycoprotein complex. These comparisons indicated that all components of the dystrophin-glycoprotein complex quantitatively coenrich

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and that the 156 kDa dystrophin-associated glycoprotein is stoichiometric with dystrophin.

Immunolocalization of dystrophin-associated proteins

5 The cellular localization of the dystrophin-associated proteins was determined by indirect immunofluorescence labeling of transverse cryostat sections of rabbit skeletal muscle. The affinity-purified polyclonal antibodies specific for the 156 kDa, 59 kDa, 50 kDa, 43 kDa and 35 kDa dystrophin-associated
10 proteins exhibited immunofluorescent staining of the sarcolemmal membrane, demonstrating the unique association of these proteins with the muscle fibre plasma membrane or the intracellular cytoskeleton subjacent to the surface membrane. All five polyclonal
15 antibodies against dystrophin-associated proteins illustrated an equal distribution between fast and slow fibers and showed enriched staining at the neuromuscular junction.

20 Example 4: Characterization of Integral Membrane Components

Alkaline extraction of the dystrophin-glycoprotein complex

25 Consistent with predictions that it is a cytoskeletal protein, dystrophin can be extracted from skeletal muscle membranes and membranes isolated from the electric organ of Torpedo californica in the absence of detergents by simple alkaline treatment. To evaluate which components of the dystrophin-glycoprotein complex are integral membrane proteins, alkaline-treated rabbit
30 skeletal muscle membranes were pelleted (100,000 x g) and the soluble supernatant and insoluble membrane pellet analyzed by SDS-polyacrylamide gel electrophoresis and

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immunoblotting. The supernatant of alkaline-treated membranes contained greater than 90% of all dystrophin while the remaining pellet-associated dystrophin could be extracted with a second alkaline treatment. The 59 kDa dystrophin-associated protein was also extracted by alkaline treatment. On the other hand, dystrophin and the 59 kDa dystrophin-associated protein remained associated with the pellet in membranes diluted in identical buffers which were not titrated to pH 11. The 156 kDa, 50 kDa, 43 kDa, and 35 kDa glycoproteins were retained in the membrane pellet after alkaline treatment. The supernatants obtained from skeletal muscle membranes titrated to pH 11, and pelleted at 100,000 x g were also enriched in non- or peripheral membrane proteins such as calsequestrin, the 53- and 160 kDa glycoproteins of the sarcoplasmic reticulum and actin, while the sarcoplasmic reticulum ryanodine receptor, an integral membrane protein, was retained in the pellet. That dystrophin and the 59 kDa dystrophin-associated protein can be extracted from skeletal muscle membranes by alkaline treatment in the absence of detergents demonstrates that these proteins are not integral membrane proteins and suggests both are elements of the cytoskeleton. These data further suggest that the 156 kDa, 50 kDa, 43 kDa and 35 kDa dystrophin-associated glycoproteins are integral membrane proteins.

Incorporation of [¹²⁵I] TID into purified dystrophin-glycoprotein complex

To further assess the hydrophobic nature of the components of the dystrophin-glycoprotein complex, the hydrophobic probe [¹²⁵I] TID was photoincorporated into purified dystrophin-glycoprotein complex. Hydrophobic segments (presumably transmembrane domains) of proteins can be specifically labeled with [¹²⁵I] TID. Dystrophin

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and the 59 kDa dystrophin-associated protein were not labeled with [125 I] TID while the 50 kDa, 43 kDa and 35 kDa dystrophin-associated glycoproteins demonstrated roughly equal incorporation of the probe. The large amount of [125 I] TID incorporation into the 25 kDa dystrophin-associated protein indicates that it is the most hydrophobic component of the complex and may explain why we have been unsuccessful in raising antibodies to it. It is not clear why the 156 kDa dystrophin-associated glycoprotein was not labeled with [125 I] TID but one explanation may be the occlusion of its transmembrane domain(s) by the other hydrophobic components of the complex.

Effect of alkaline treatment on immunoprecipitation of the dystrophin-glycoprotein complex

It has been demonstrated that the components of the purified dystrophin-glycoprotein complex no longer co-sediment on sucrose density gradients after alkaline dissociation. While dystrophin, the 156 kDa and 59 kDa dystrophin-associated proteins exhibited distinct sedimentation peaks after alkaline dissociation, the 50 kDa, 43 kDa and 35 kDa dystrophin-associated glycoproteins appeared to cosediment as a complex. To determine whether the 50 kDa, 43 kDa and 35 kDa dystrophin-associated glycoproteins remains complexed after immunoprecipitation by mAb XIXC2 (dystrophin)-Sepharose or mAb IVD3₁ (50 kDa glycoprotein)-Sepharose was analyzed by SDS-polyacrylamide gel electrophoresis and immunoblotting. Both the dystrophin- and 50 kDa dystrophin-associated glycoprotein-antibody matrices were effective in immunoprecipitating greater than 99% of dystrophin and 96% of the 59 kDa, 50 kDa, 43 kDa and 35 kDa dystrophin-associated proteins from untreated dystrophin-glycoprotein complex. Dystrophin- and 50 kDa

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dystrophin-associated glycoprotein- antibody matrices immunoprecipitated 63% and 85% of the 156 kDa dystrophin-associated glycoprotein. The dystrophin-antibody matrix immunoprecipitated greater than 99% of the dystrophin
5 from the alkaline-treated dystrophin-associated proteins and only 51% of the 59 kDa dystrophin-associated protein indicating that the interaction between dystrophin and the complex was disrupted by alkaline treatment. The 50 kDa dystrophin-associated glycoprotein-antibody matrix
10 immunoprecipitated less than 25%, 32% and 43% of dystrophin-associated proteins from the alkaline-treated complex. However, 96% of the 50 kDa, 43 kDa and 35 kDa dystrophin-associated glycoproteins were immunoprecipitated from the alkaline-treated complex
15 using the 50 kDa dystrophin-associated glycoprotein antibody matrix. Thus, these data demonstrate that the 50 kDa, 43 kDa and 35 kDa dystrophin-associated proteins alone form a tightly-associated complex. Since the 50 kDa dystrophin-associated glycoprotein-antibody matrix
20 immunoprecipitates more of the 156 kDa dystrophin-associated glycoprotein than the dystrophin-antibody matrix, these data further suggest that the 156 kDa dystrophin-associated glycoprotein is directly linked to the 50 kDa, 43 kDa and 35 kDa glycoprotein complex rather
25 than to dystrophin.

Example 5: Dystrophin-Associated Protein
 Expression in Normal and Dystrophic
 Murine Skeletal Muscle

Isolation of skeletal and cardiac muscle membranes

30 Skeletal and cardiac muscle membranes were prepared from age-matched normal control mice and mdx mice. During the isolation procedure, membrane preparations from different mice were not combined but kept separate

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for comparative purposes. Hind leg and back muscle were dissected as quickly as possible and homogenized in 7.5 volumes of homogenization buffer by a Polytron (Kinematic GmbH, Luzern, Switzerland) in the presence of a protease inhibitor cocktail to minimize protein degradation (see Ohlendieck et al., J. Cell. Biol. 112: 135-148 (1991)). Homogenates were centrifuged for 15 min at 3,000 x g and the supernatant filtered through 4 layers of cheese cloth. The pellets from this initial centrifugation step were re-homogenized and centrifuged as above and the supernatants of four repeated homogenization cycles combined. Membrane pellets were obtained by centrifugation of the combined supernatants for 35 min at 140,000 x g and the final preparation was KCl-washed as described by Ohlendieck et al., J. Cell Biol. 112:135-148 (1991). Cardiac membranes from control and dystrophic dy/dy mice (C57BL/6J-dy; Jackson Laboratory, Bar Harbor, Maine) were prepared as described for control and mdx mouse muscle.

A newly established wheat germ agglutination procedure was employed to isolate purified skeletal muscle sarcolemma (see Ohlendieck et al. J. Cell Biol. 112:135-148 (1991)) and dystrophin-glycoprotein complex was prepared from rabbit skeletal muscle as described by Ervasti et al., (Nature 345:315-319 (1990)). Protein was determined as described by Peterson (Anal. Biochem. 83:346-356 (1977)) using bovine serum albumin as a standard.

Preparation of sheep antisera using native complex immunogen

Monospecific antibodies against the different components of the dystrophin-glycoprotein complex were produced by injecting the native dystrophin-glycoprotein complex purified as described herein into sheep. After

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testing the crude sheep antisera for the presence of antibodies against the dystrophin-glycoprotein complex, monospecific antibodies to 35 kDa glycoprotein, 43 kDa glycoprotein, 50 kDa glycoprotein and 59 kDa protein were
5 affinity purified from individual immobilon strips of the various components of the dystrophin-glycoprotein complex as described by Sharp *et al.*, (*J. Biol. Chem.* 264:2816-2825 (1989)). Specificity of affinity-purified antibodies was subsequently determined by immunoblot
10 analysis with rabbit sarcolemma and rabbit dystrophin-glycoprotein complex.

Monoclonal antibodies XIXC1 to dystrophin, VIA41 to 50 kDa glycoprotein, McB2 to Na/K-ATPase (Urayama *et al.*, *J. Biol. Chem.* 264:8271-8280 (1989)) and IID8 to cardiac
15 Ca^{2+} -ATPase (Jorgensen *et al.*, *Cell Motil Cytoskel.* 9:164-174 (1988)) were previously characterized by extensive immunofluorescence and immunoblot analysis (Ohlendieck *et al.*, *J. Cell Biol.* 112:135-148 (1991)). Rabbit polyclonal antibodies against the C-terminal
20 sequences of human dystrophin and human dystrophin-related protein (DRP) were affinity-purified and characterized as described (Ervasti *et al.*, *J. Biol. Chem.* 266:9161-9165 (1991)). Monoclonal antibody SB-SP-1 against spectrin was purchased from Sigma Chemical
25 Company (St. Louis, MO).

Gel electrophoresis and immunoblot analysis

Proteins were fractionated on 3-12% gradient SDS polyacrylamide gels and protein bands were visualized by Coomassie-blue staining and also analyzed by Stainsall
30 staining. Proteins were transferred to nitrocellulose and immunoblot staining with antibodies and densitometric scanning was carried out as described above. Both protein A and protein G did not label primary sheep antibody sufficiently. Therefore, after primary labeling

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with sheep antibody, immunoblots of mouse muscle membranes were incubated with rabbit anti-sheep secondary antibody followed by incubation with ^{125}I -labeled protein A (Amersham Corporation). This procedure gave
5 reproducibly a very strong signal in autoradiography and enabled densitometric scanning of DAP antibody binding to control and mdx mouse muscle membranes.

Lectin-staining of immunoblots was carried out under optimized conditions as described (Campbell et al.,
10 Nature 338:259-262 (1989); Ohlendieck et al., J. Cell Biol. 112:135-148 (1991)). Blots were incubated for 1 hr with 1:1,000 diluted peroxidase-labeled wheat germ agglutinin, concanavalin A and jacalin (Vector Laboratories, Burlingame, CA) and developed in 20 mM
15 Tris-Cl, pH 7.5, 200mM NaCl using 4-chloro-1-naphthol as substrate (Jorgensen et al., J. Cell Biol. 110:1173-1185 (1990)).

Immunofluorescence microscopy

Immunofluorescence microscopy of 8 μm transverse
20 cryosections from control, mdx and dy/dy mouse skeletal muscle was performed as described by Ohlendieck et al. (J. Cell Biol. 112: 135-148 (1991)). Following preincubation for 20 min with 5% normal goat antiserum in PBS (50 mM sodium phosphate, pH 7.4, 0.9% NaCl),
25 cryosections were incubated for 1 hr at 37°C with primary antibodies (1:1,000 dilution of crude antisera or 1:100 dilution of hybridoma supernatant or 1:50 dilution of affinity-purified antibodies). After extensive washing in PBS the sections were labeled with 1:100 diluted
30 affinity-purified fluorescein-labeled goat anti-mouse IgG or goat anti-rabbit IgG (Boehringer-Mannheim) and subsequently examined in a Zeiss Axioplan fluorescence microscope. In the case of mouse monoclonal antibodies used on mouse cryosections, a biotin-streptavidin system

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was employed for immunodetection. Affinity-purified primary antibodies were biotinylated according to the instructions in the commercially available biotinylation kit from Amersham Corporation. Cryosections were

5 incubated with biotinylated primary antibody as already described for unlabeled primary antibody and subsequently extensively washed in PBS. Finally, sections were fluorescently labeled by incubation with 1:100 diluted affinity-purified fluorescein-conjugated avidin (Sigma

10 Chemical Company).

For labeling of skeleton muscle specimen with wheat germ agglutinin (WGA), cryosections were incubated with 1:2,000 diluted fluorescein-conjugated WGA (Sigma Chemical Company) for 30 min in the presence and absence

15 of 0.3 M N-acetyl-glucosamine. Sections were intensively washed in PBS and then examined for specific labeling in a fluorescence microscope. Histochemical examination of control, mdx and dy/dy mouse skeletal muscle cryosections was performed by haematoxylin and eosin staining as

20 described by Dubowitz (Muscle Biopsy - A Practical Approach, London:Bailliere Tindall, 1985, 2d edition).

Immunofluorescence microscopy of biopsy specimens from patients afflicted with neuromuscular disorders was performed under identical conditions. Cryosections from

25 healthy normal humans of varying age and sex and cryosections from patients suffering from a variety of different neuromuscular disorders (Duchenne muscular dystrophy, Becker's muscular dystrophy, limb girdle dystrophy, congenital muscular dystrophy and spinal

30 muscular atrophy) were placed on the same microscopy slide and the samples therefore treated in an identical manner during all incubation and washing steps. Human muscle biopsy specimen were obtained from the Departments of Pediatrics and Neuropathology, University of Iowa

35 Clinics and Hospitals.

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Immunoblot analysis of antibodies to dystrophin-associated proteins

Sheep antiserum raised against the native dystrophin-glycoprotein complex was used to affinity-purify monospecific antibodies to the individual components of the tightly associated dystrophin-glycoprotein complex. The high specificity of the eluted, affinity-purified antibodies was demonstrated by immunoblot. Sheep antibodies to 35 kDa glycoprotein, 43 kDa glycoprotein, 50 kDa glycoprotein and 59 kDa protein exhibited strong labeling of their respective antigen in sarcolemma and isolated dystrophin-glycoprotein complex from rabbit skeletal muscle. These results indicate monospecificity of the affinity-purified antibodies for the different components of the dystrophin-glycoprotein complex and this is a crucial prerequisite for the characterization of components of the complex in control, mdx and dy/dy muscle. Sheep antibodies to 156 kDa glycoprotein did not exhibit strong labeling in immunoblotting and furthermore the affinity-purification of sheep antibodies to 156 kDa glycoprotein is complicated due to contaminating fragments from degraded dystrophin molecules. We therefore used the already previously characterized monoclonal antibody VIA4₁ for the analysis of 156 kDa glycoprotein, which is a highly specific probe and exhibits strong labeling in immunoblotting.

Dystrophin-associated proteins in skeletal muscle membranes from mdx mouse

After characterization, the affinity-purified sheep antibodies were used in an extensive immunoblot analysis to compare the expression of components of the dystrophin-glycoprotein complex in skeletal muscle membranes from control and mdx mouse. Mdx mouse is a

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possible animal model from Duchenne muscular dystrophy which is missing dystrophin due a point mutation in the dystrophin gene. Skeletal muscle fibers from mdx mouse undergo cycles of degeneration and regeneration and it is
5 therefore of considerable interest to examine the status of dystrophin-deficient mdx skeletal muscle. Coomassie-blue and "Stains-all" staining reveals that membrane preparations from control and mdx mouse skeletal muscle are similar in composition. Crude skeletal muscle
10 membranes from mdx mouse are characterized by the absence of dystrophin but contain dystrophin-related protein in normal size and abundance as already previously described for purified sarcolemma.

Prior to the examination of the dystrophin-
15 associated glycoproteins in mdx mouse muscle the general status of glycoproteins and sarcolemma components in the membrane preparation of mdx muscle used in this study was evaluated. It is important to account for possible secondary effects to proteins caused by the ongoing
20 degeneration and regeneration cycles in mdx skeletal muscle fibers. Lectin-staining with wheat germ agglutinin-concanavalin A and jacalin showed that the glycoprotein composition with respect to these three lectins is very comparable in control and mdx mouse
25 muscle membranes. Furthermore, plasma membrane marker Na/K-ATPase was found to be equally distributed in both membrane preparations. These results indicate that the general glycoprotein and sarcolemma protein composition is not severely affected in mdx mouse muscle.

30 Identical immunoblots were examined for the relative expression of dystrophin-associated proteins in skeletal muscle membranes from control and mdx mouse. The relative abundance of dystrophin-associated proteins of apparent 35 kDa, 43 kDa, 50 kDa, 59 kDa and 156 kDa
35 proteins is greatly reduced in mdx muscle membranes.

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Densitometric scanning of ^{125}I -protein A-labeled immunoblots, carried out as described above, revealed a 84 ± 3 reduction for 35 kDa glycoprotein, 80 ± 5 reduction for 43 kDa glycoprotein, 83 ± 5 reduction for 50 kDa glycoprotein, 86 ± 6 reduction for 59 kDa protein and approximately 80-90% reduction for 156 kDa glycoprotein in mdx muscle membranes when compared to control membranes. The comparative densitometric scanning was performed with individually isolated from five 10-week old control mice and five-week old mdx mice. A similarly reduced expression of dystrophin-associated proteins was also observed in membranes isolated from 5, 20 and 30-week old mdx mice as compared to age-matched control mice. The same results were obtained with crude skeletal muscle membranes, which had not been washed with 0.6 M KCl, and also with microsomal membranes prepared as described by Ohlendieck *et al.*, *J. Cell. Biol.* **112**:135-148 (1991). These findings indicate that mdx mouse skeletal muscle are not only deficient in dystrophin, but that in addition the density of the dystrophin-associated glycoproteins is greatly reduced in mdx mouse muscle.

Dystrophin-associated proteins in skeletal muscle membranes from dy/dy mouse

Dystrophic skeletal muscle fibers from the animal model dy/dy mouse have a similar histochemical appearance to skeletal muscle fibers in human muscular dystrophy. However, the genetic locus for the neuromuscular disorder dystrophia muscularis was assigned to mouse chromosome 10. Muscle membranes from dy/dy mouse contain dystrophin of normal size and abundance making this animal model a very good control for the status of dystrophin-associated proteins in necrotic, but dystrophin-containing muscle tissue. Coomassie-blue staining revealed no apparent differences between membranes isolated from control and

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dy/dy mouse skeletal muscle and the density of dystrophin-related protein is also comparable between both membrane preparations. Most importantly, antibodies to the different dystrophin-associated proteins showed approximately equal amounts of these proteins in skeletal muscle membranes from control and dy/dy mouse. These findings demonstrate that dystrophin-associated proteins are not affected by secondary events in necrotic dy/dy muscle which contains dystrophin. Therefore, the reduced expression of dystrophin-associated proteins in skeletal muscle membranes from mdx mice is most likely a primary event following the absence of dystrophin from the membrane cytoskeleton of mdx muscle.

Example 6: Distribution of Dystrophin-Associated Proteins in Normal and Dystrophic Human Tissue

The results disclosed in Example 5 demonstrate the absence, or dramatic reduction in the abundance of, dystrophin-associated proteins in tissue samples from dystrophic mice. The present example discloses a similar finding in human tissue samples by immunofluorescence microscopy and immunoblot analysis.

Biopsy Specimens

Skeletal muscle biopsy specimens were obtained from original diagnostic specimens or discarded surgical material with the approval of the institutional review board for medical projects of the University of Iowa Hospitals and Clinics. Normal human skeletal muscle was obtained from the Department of Surgery, University of Iowa Hospitals and Clinics during routine surgical procedures involving different muscles from twenty individuals (6-70 years old) who had no clinical history

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of neuromuscular disorders. The analysis carried out in the present Example comprised skeletal muscle specimens from 12 DMD patients (3-14 years old) of the University of Iowa Hospitals and Clinics.

5 Cardiac DMD muscle was obtained at Texas Children's Hospital, Baylor College of Medicine from a 12 year old boy. For comparative purposes, a large number of muscle samples from patients afflicted with other neuromuscular disorders were investigated. These samples were obtained
10 from patients seen in the Adult and Pediatric Neuromuscular Clinics at the University of Iowa Hospitals and Clinics. Besides the routine histopathological diagnosis, muscle biopsy specimens from patients
15 afflicted with neuromuscular disorders were tested for dystrophin. Patient biopsy specimens were quick-frozen in liquid nitrogen-cooled isopentane and stored frozen at -80°C until use.

Immunofluorescence Microscopy

Immunofluorescence microscopy of 7 μ m cryosections
20 from human skeletal muscle specimens was performed as previously described for rabbit muscle. Antibodies used in the experiments described in this Example were from various sources. Monoclonal antibody (mAb) IVD31 to 50-DAG, mAb IIH6 to 156-DAG, mAbs VIA42 and XIXC2 to
25 dystrophin were produced and characterized as described previously. The antibodies to dystrophin do not immunologically cross-react with spectrin, α -actin or dystrophin-related protein and furthermore stain
30 exclusively the sarcolemma of normal human and mouse muscle cryosections, but not DMD or mdx mouse muscle cells, which are lacking dystrophin. Therefore the antibodies used in this investigation are specific probes for human dystrophin which is an important prerequisite for the diagnosis of Duchenne muscular dystrophy and

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related neuromuscular disorders. Highly specific antibodies against the dystrophin-glycoprotein complex were raised in sheep using the purified dystrophin-glycoprotein complex. Antibodies to the individual components of the dystrophin-glycoprotein complex were affinity-purified from individual Immobilon-P transfer membrane strips as described. While satisfactory immunoblot and immunofluorescence staining of muscle membranes and cryosections from normal and mdx mice was obtained with the serum taken after the first booster injection (see Example 5), human muscle membranes and cryosections were labeled much more strongly by sheep serum taken after a further booster injection with purified dystrophin-glycoprotein complex. Rabbit antibodies to the last 12 amino acids of the C-terminus of dystrophin-related protein (DRP) were previously characterized and do not immunologically cross-react with dystrophin. Monoclonal antibody SB-SP-1 to spectrin was purchased from Sigma Chemical Company.

Depending on the secondary antibodies used, cryosections of skeletal muscle were pre-incubated for 20 min with 5% normal goat serum in PBS (50 mM sodium phosphate, pH 7.4, 0.9% NaCl) or 5% normal rabbit serum in PBS supplemented with 5% bovine serum albumin. Subsequently cryosections were treated in a 1-h incubation at 37°C with different dilutions of primary antibody. After washing in PBS sections were labeled at 37°C with 1:200 diluted affinity-purified fluorescein-labeled goat anti-mouse IgG (Boehringer-Mannheim) and subsequently examined in a Zeiss Axioplan fluorescence microscope. In the case of primary sheep antibodies, cryosections were washed in PBS and then incubated for 30 min at 37°C with 1:500 diluted biotinylated rabbit anti-sheep IgG (Vector Laboratories). Finally, after washing in PBS cryosections were labeled

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for 30 min at 37°C with 1:1000 diluted fluorescein-conjugated avidin (Sigma Chemical Company). For labeling of skeletal muscle specimens with wheat germ agglutinin (WGA) cryosections were incubated with 1:1,000
5 diluted fluorescein-conjugated WGA (Sigma Chemical Company) for 30 min in the presence and absence of 0.3 M N-acetyl-glucosamine.

Prior to the characterization of dystrophin-associated proteins in DMD patients, all human
10 skeletal muscle cryosections used in this investigation were characterized by labeling with antibodies to dystrophin and spectrin, as well as stained with wheat germ agglutinin. In contrast to dystrophin, which is completely missing in DMD skeletal muscle, it was found
15 that the membrane cytoskeletal protein spectrin labels evenly the cell periphery of skeletal muscle fibers from DMD patients. Because this investigation evaluates the status of sarcolemmal glycoproteins the overall wheat germ agglutinin (WGA) staining of different muscle
20 specimens was also examined. Both normal human and DMD skeletal muscle exhibited strong WGA-labeling of the cell periphery, which could be specifically eliminated by pre-incubation with the competitive sugar
N-acetyl-glucosamine. In addition to muscle cell surface
25 staining, normal and especially DMD skeletal muscle showed strong lectin binding to the endomysial and perimysial connective tissue. These findings indicate that the majority of WGA-binding components of the skeletal muscle cell periphery are not affected in DMD.
30 This is important in analyzing of the status of dystrophin-associated glycoproteins in DMD muscle. In addition, it was previously shown that no general depletion of plasma membrane glycoproteins occurs in DMD skeletal muscle.

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Sheep antibodies to the individual components of the dystrophin-glycoprotein complex, the specificity of which was previously characterized in normal and mdx mouse muscle, were used to evaluate the status of

5 dystrophin-associated proteins in muscle biopsy specimens from DMD patients. Immunofluorescence staining revealed restricted labeling of dystrophin-associated proteins to the cell periphery of normal human muscle fibers. Skeletal muscle cryosections exhibited no staining of the

10 interior of myofibers suggesting a specific association of dystrophin-associated proteins with the sarcolemma membrane of human skeletal muscle. This was previously established for mouse and rabbit skeletal muscle using subcellular fractionation studies and immunofluorescence

15 microscopy. In order to reliably compare all muscle biopsy specimens, cryosections were all placed on the same microscopy slide, labeled with the same concentration of primary and secondary antibodies and were treated in an identical way during all incubation

20 and washing steps. Undiluted affinity-purified sheep antibodies in combination with a biotin-streptavidin system were used for immunodetection. Photographs were taken under identical conditions with the same exposure time so that a direct comparison of immunofluorescence

25 staining intensity could be undertaken. The immunofluorescence analysis of the DMD skeletal muscle specimen reveals the general loss of dystrophin-associated glycoproteins in all 12 DMD

30 patients investigated. Histological examination of DMD skeletal muscle, stained with hematoxylin and eosin, showed severe dystrophic degeneration with a rounded contour of muscle cells, central nucleation, a marked variability of fiber size diameter, scattered necrotic muscle fibers and increased interstitial fibrosis typical

35 for DMD muscle. While the cell periphery of DMD skeletal

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muscle specimens exhibits normal amounts of spectrin, strong staining for WGA in interstitial connective tissue and a complete lack of dystrophin, it exhibits a drastic loss of 156-DAG, 59-DAP, 50-DAG, 43-DAG and 35-DAG. This was observed in all DMD muscle fibers and did not correlate with the severity of degeneration of individual skeletal muscle fibers. However it should be noted that immunofluorescence staining is not only reduced, but the muscle cell periphery is discontinuously labeled in a patchy fashion. In stark contrast to DMD, dystrophin-associated proteins exhibited normal immunofluorescence labeling of the skeletal muscle cell periphery from patients suffering from limb girdle dystrophy, congenital muscular dystrophy and spinal muscular atrophy. These results demonstrate that a deficiency in dystrophin in human DMD skeletal muscle is accompanied by a specific and substantial reduction in all of the dystrophin-associated proteins.

The results obtained with affinity-purified sheep antibodies to 50-DAG were confirmed by immunofluorescence microscopy with monoclonal antibody IVD31 against 50-DAG. A 1:100 dilution of IVD31 hybridoma supernatant produced satisfactory results. Biopsy specimens from DMD patients of varying ages exhibited very low levels of immunofluorescence staining intensity for 50-DAG when directly compared to normal age-matched human muscle. Similar to the results obtained with affinity-purified sheep antibodies, immunofluorescence staining with mAb IVD31 varied in the degree of reduction between individual DMD cases. Besides drastic reduction of immunofluorescence staining intensity, labeling of 50-DAG was observed to be discontinuous in the skeletal muscle cell periphery of DMD patients.

To investigate the status of 50-DAG in necrotic muscle fibers which show no deficiency in dystrophin,

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specimens from a variety of other neuromuscular disorders were labeled with mAb IVD31. 50-DAG was found in normal amounts in the cell periphery of muscles from patients afflicted with limb girdle dystrophy, congenital muscular dystrophy and spinal muscular atrophy. Biopsy specimens from two patients suffering from facioscapulohumeral muscular dystrophy and a patient afflicted with Friedreich's ataxia also exhibited normal immunofluorescence labeling of the muscle cell periphery for 50-DAG. These are important findings because they suggest that dystrophin-associated glycoproteins are not severely affected by secondary effects in muscle fiber degradation. The loss of dystrophin-associated proteins appears to be directly related to a deficiency in the cytoskeletal component dystrophin and was observed in all DMD skeletal muscle fibers independent of the severity of muscle degeneration.

Immunoblot analysis of total human muscle membranes

In order to quantitate the remaining amounts of dystrophin-associated proteins in DMD skeletal and cardiac muscle membranes, immunoblot analysis of total muscle membranes was carried out. Total SDS muscle extracts are routinely used to evaluate the status of the high molecular weight component dystrophin and 156 kDa dystrophin-associated protein in patients. In contrast, total SDS-extracts are not suitable for the study of low molecular weight proteins due to the high density of low molecular weight muscle proteins. Therefore a total membrane fraction of skeletal and cardiac muscle was used to investigate the low molecular weight components of the dystrophin-glycoprotein complex. In addition, an obvious difficulty in studying dystrophin-associated glycoproteins in DMD muscle membranes was the very restricted amount of muscle tissue obtainable from

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diagnostic biopsies. This problem was overcome by acquiring 2-5 grams of DMD muscle (cardiac and skeletal) during spinal fusion surgery. After arrival in the laboratory the tissue was washed in ice-cold

5 phosphate-buffered saline and then immediately processed for centrifugation. The starting material for preparations of cardiac membranes was approximately 1g of human heart samples. Control cardiac muscle included explanted heart tissue from a transplant patient and a

10 cardiac autopsy specimen from another individual obtained shortly after death. Muscle samples were homogenized and centrifuged in 7.5 volumes of 20 mM sodium pyrophosphate, 20 mM sodium phosphate monohydrate, .1 mM $MgCl_2$, 0.303 M sucrose, 0.5 mM EDTA, pH 7.0 at 1,100 xg as described in

15 Example 5. All buffers used were supplemented with a protease inhibitor cocktail to prevent protein degradation. To obtain total membranes, supernatants were filtered through cheese cloth and centrifuged at 135,000 xg for 37 min. Samples were stored in small

20 aliquots at $-135^{\circ}C$ until use. Protein concentration was determined using bovine serum albumin as standard. Membrane proteins were fractionated on 3-11% gradient SDS polyacrylamide gels and transferred to nitrocellulose membranes. Immunoblot staining with antibodies and

25 densitometric scanning of radioactively labeled immunoblots was performed as described previously.

DMD skeletal muscle membranes exhibited increased amounts of dystrophin-related protein but lacked dystrophin. Staining with peroxidase-conjugated lectins

30 (wheat germ agglutinin, concanavalin A, jacalin) did not show differences in the major glycoprotein composition of both membrane preparations. Coomassie-blue staining revealed a comparable overall protein composition of normal and DMD skeletal muscle membranes. However, all

35 of the dystrophin-associated proteins were found to be

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reduced in DMD skeletal muscle membranes when compared to a membrane preparation from age-matched normal human muscle. Densitometric scanning of identical immunoblots which were labeled with ^{125}I -labeled Protein-A revealed

5 an approximately 90% reduction for all of the dystrophin-associated proteins in DMD skeletal muscle membranes. The reduction of dystrophin-associated proteins in muscle membranes from DMD patients observed in immunoblotting confirms the finding of a lower density

10 of all of the dystrophin-associated proteins in DMD skeletal muscle cryosections. The fact that dystrophin-associated proteins are detectable in the DMD muscle cell periphery by immunofluorescence microscopy and in DMD muscle membranes by immunoblotting suggests

15 that remaining dystrophin-associated proteins are not present in the cytoplasm but are localized to the sarcolemma membrane and are not degraded.

After establishing the reduction of dystrophin-associated proteins in cryosections and total

20 membranes from DMD skeletal muscle, the status of the individual components of the dystrophin-glycoprotein complex in cardiac DMD muscle was also investigated. Antibodies to dystrophin-associated proteins did not exhibit satisfactory immunofluorescence labeling of human

25 cardiac muscle thus we were not able to investigate their status in cardiac DMD cryosections.

Total membranes from normal human and DMD cardiac specimens were separated by 3-12% SDS-PAGE and analyzed by immunoblotting. Normal human cardiac muscle contains

30 all of the components of the dystrophin-glycoprotein complex as previously found for rabbit skeletal muscle. Cardiac DMD muscle membranes, which completely lacked dystrophin, exhibited near to normal amounts of dystrophin-related protein. By contrast all of the

35 dystrophin-associated proteins were greatly reduced and

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this is analogous to the findings in skeletal muscle membranes from DMD patients. Densitometric scanning of ^{125}I -labeled Protein-A immunoblots showed approximately 90% reduction for all of the dystrophin-associated proteins in human cardiac DMD muscle. Immunoblot analysis of two patients afflicted with inherited cardiomyopathy showed similar amounts of all of the components of the dystrophin-glycoprotein complex when directly compared to normal human cardiac muscle. In summary, immunoblotting of total muscle membranes enabled the quantitation of the remaining amounts of the individual components of the dystrophin-glycoprotein complex in skeletal and cardiac DMD muscle. The immunoblot data agrees with the results from immunofluorescence microscopy that all of the dystrophin-associated proteins are dramatically reduced in DMD muscle.

Example 7: Primary Structure of the 43 kDa and 156 kDa Dystrophin-Associated Proteins

The primary sequence of two dystrophin-associated proteins has been established by cDNA cloning and DNA sequencing. In this Example, it is shown that the transmembrane 43 kDa and extracellular 156 kDa dystrophin-associated glycoproteins are encoded by a single mRNA and that the extracellular 156 kDa DAG binds laminin.

Cloning and primary sequence analysis of a precursor protein for the 43/156 kDa DAG

Affinity purified guinea pig polyclonal antibodies to the 43 kDa DAG were prepared as described by Ervasti and Campbell, Cell 66:1121-1131 (1991)) and used to screen 2×10^6 clones of λ gt11 expression library. Clone R43-A with a length of 600 base pairs was isolated from a

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random primed adult rabbit skeletal muscle λ gt11 library by immunoscreening. An oligo-dT primed rabbit skeletal muscle cDNA library in λ zapII (Stratagene) was screened at high stringency with a ^{32}P -labelled cDNA insert from the R43-A clone (random primed labelling kit, Boehringer Mannheim Biochemicals). Clone R43-B overlaps R43-A and extends 1 kb in the 5' direction. Further clones were isolated from λ gt11 libraries: R43-D - random primed λ gt11 library, R43-C - oligo-dT primed λ gt11 library. To isolate cDNA extending to the 5'-end of mRNA (clone R43-E), a rabbit skeletal muscle cDNA library was constructed using random primed cDNA with λ gt11 vector (Stratagene). All cDNA inserts were sequenced either on an Applied Biosystems Incorporated Automatic Sequencer or manually by the dideoxy chain termination method. Sequences were analyzed with the Genetics Computer Group Inc. (Wisconsin package) and PCGene (Intelligenetics) Software.

The 4200 nucleotide cDNA shown in the SEQ ID NO: 1 sequence contains a 2685 nucleotide open reading frame (beginning at nucleotide 170) coding for a polypeptide of 895 amino acids with a calculated molecular mass of 97,029. The first 29 amino acids of the open reading frame are predominantly hydrophobic and likely represent a signal peptide. Hydropathy analysis identified a single continuous region of 24 amino acids close to the C-terminal showing characteristics of a transmembrane domain. Four potential N-linked glycosylation sites and numerous potential phosphorylation sites are found in the 97 kDa polypeptide. Finally, no significant sequence homology was detected in the NBRF database between any known proteins and the predicted amino acid sequence of the 97 kDa polypeptide.

Biochemical characterization of the dystrophin-glycoprotein complex has demonstrated that the

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43 kDa DAG has hydrophobic properties characteristic of a transmembrane protein and contains Asn-linked oligosaccharides. These properties are consistent with the predicted sequence of the C-terminal half of the 97 kDa polypeptide which contains a potential transmembrane domain and three out of four potential sites for N-glycosylation. The C-terminal origin of 43 kDa DAG was confirmed using an antibody raised in a rabbit against a synthetic peptide corresponding to the 15 C-terminal amino acid residues of the deduced sequence. This anti-peptide antibody specifically recognized the 43 kDa DAG. In addition, peptide sequence determined directly from the 43 kDa DAG matched 783-793 residues of the deduced amino acid sequence of the 97 kDa polypeptide.

15 N-terminal domain of the 97 kDa precursor encodes 156 kDa DAG

In order to identify the N-terminal domain of the 97 kDa precursor polypeptide, antibodies to different regions of the 97 kDa precursor polypeptide were produced by expressing several overlapping cDNAs encoding different regions in the 97 kDa precursor polypeptide. A set of pGEX vectors (Smith and Johnson, Gene 67:31-40, (1988)) were used to express various fragments of DNA for 97 kDa precursor protein as E. coli fusion proteins.

25 Fusion protein-A (FP-A) contains residues 665-856 corresponding to the cDNA R43-A found in the expression library with affinity-purified antiserum against 43 kDa DAG. Fusion protein-C (FP-C) contains residues 857-895 which are the C-terminal 38 amino acids of the 97 kDa precursor polypeptide, and does not overlap with FP-A.

30 Fusion protein-B (FP-B) contains residues 367-863 and thus overlaps with FP-A and FP-C, and has a portion of the N-terminal region of the 97 kD precursor, which is not present in the mature 43 kDa DAG. Fusion protein-D

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(FP-D) contains residues 62-438 and thus contains only the N-terminal region of the 97 kDa precursor polypeptide. The correct construction of the recombinant plasmids was verified by restriction mapping. To

5 construct FP-A, the EcoRI insert from R43-A clone with the size of 0.6 kb was cloned into the EcoRI site of pGEX-1. FP-B was constructed by ligation EcoRI insert from R43-B clone (1.5 kb) into the EcoRI site of pGEX-2T. FP-C was made by ligation into the BamHI site of pGEX-1

10 the BamHI fragment of cDNA R43-C, containing C-terminal sequence with stop codon, representing last 38 amino acids. For the FP-D construct, EcoRI insert (1.2 kb) from R43-D was inserted into pGEX-2T vector digested with EcoRI.

15 Each recombinant molecule was introduced in *E. coli* DH5a cells. Overnight cultures were diluted 1:10, incubated for one hour and induced for 2 hours with 1mM IPTG. Cells were resuspended in PBS and sonicated. Fusion proteins were purified from supernatant by affinity

20 chromatography on glutathione-Sepharose (Pharmacia) and eluted with 5 mM glutathione. Dystrophin-glycoprotein complex was isolated as described Lesot *et al.* (*Cell* 66:1121-1131 (1991)). Sheep polyclonal antibodies to the purified DGC were produced as described Ohlendieck and

25 Campbell (*J. Cell Biol.* 115:1685-1694 (1991)) and anti-fusion protein antibodies were affinity purified from polyclonal antiserum. A peptide representing the 15 carboxyl-terminus amino acids of the 97 kDa cDNA (PKNMTPYRSPPPYVP) was obtained from the HHMI Peptide

30 Facility (Washington University, St. Louis) as the N-terminal p-benzoylbenzoyl-peptide photoprobe. Peptide was conjugated to keyhole limpet hemocyanin, mixed with Freund's complete adjuvant and injected into a rabbit as immunogen. SDS-PAGE was carried out on 3-12% gradient

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gels in the presence of 1% 2-mercaptoethanol and transferred to nitrocellulose for immunoblot analysis.

Affinity-purified antibodies were then tested using each fusion protein and purified DGC. Consistent with the C-terminal domain encoding the 43 kDa DAG, antibodies to FP-A and FP-C specifically stained both bands of 43 kDa DAG doublet. However, antibodies to FP-B stained the 43 kDa DAG and the 156 kDa DAG components of DGC. Thus, a second product of 97 kDa precursor polypeptide appears to be the 156 kDa DAG. In accordance with this supposition, antibodies to FP-D stain only 156 kDa DAG. Therefore, posttranslational processing of 97 kDa precursor polypeptide gives rise to two components of DGC: 43 kDa DAG and 156 kDa DAG. Biochemical studies have demonstrated that 156 kDa DAG is not an integral membrane protein and contains N-linked and O-linked glycosylation. These properties are consistent with the predicted N-terminal half of the 97 kDa precursor which does not possess any hydrophobic region, has one potential N-linked glycosylation site and many potential O-glycosylation sites.

Expression of 43/156 kDa DAG in muscle and non-muscle tissues

Tissue distribution of 43/156 kDa DAG was examined by Northern blot analysis. Total RNA was isolated by homogenization in RNazol (Cinna/Biotech, TX) followed by chloroform extraction. Poly(A) RNA was enriched by oligo-dT cellulose chromatography and resolved on 1.2% agarose gels containing 5% formaldehyde. RNA was transferred to Genescreen Nylon Membranes (NEN Research Products, MA). Prehybridization was performed at 42°C in 5x SSC, 5x Denhardt's solution, 50% formamide, 10% dextran sulfate and 100 µg/ml of salmon sperm DNA. Probes were hybridized overnight at 42°C at a specific

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activity of at least 1×10^6 cpm/ml. Membranes were washed at 62°C in 2 x SSC, 0.1% SDS and were exposed to film (X-OMAT AR, Kodak) at -80°C .

5 A prominent 5.8 kb transcript was detected in mRNA from rabbit skeletal muscle, cardiac muscle and lung. A weaker hybridizing transcript of the same size was found in brain. Northern blot analysis with total RNA from variety of tissues: liver, kidney, diaphragm and stomach also detected a 5.8 kb mRNA in all these tissues. Thus, 10 the 5.8 kb transcript for the 43/156 kDa DAG is present in various muscle and non-muscle tissues, most likely originating from the same gene.

Identification of the 43/156 kDa DAG in muscle and non-muscle tissues was performed using immunoblots of 15 membranes from different tissues and affinity-purified antibodies to FP-B (43/156 kDa specific). Total membranes were prepared from tissues homogenized in 7.5 volumes of homogenization buffer (20 mM sodium pyrophosphate, 20 mM sodium phosphate monohydrate, 1 mM 20 MgCl_2 , 0.3 M sucrose, 0.5 mM EDTA, pH 7.0) using a Polytron PTS-10-S probe (Kinematic GmbH, Luzern, Switzerland) in the presence of a protease inhibitor cocktail. Homogenates were centrifuged for 15 min at $1100 \times g$ and the supernatant filtered through cheese 25 cloth. The supernatants of four repeated homogenizations were combined and centrifuged for 35 min at $140,000 \times g$. The final membrane preparations were KCl-washed as previously described. Immunoblot analysis was performed as previously using 250 μg of skeletal muscle membranes 30 and 500 μg of non-muscle membranes.

The 43 kDa DAG was detected in isolated membranes from skeletal muscle, brain, cardiac muscle and lung. The 156 kDa DAG was detected in skeletal and cardiac muscle membranes, but was slightly lower in molecular 35 weight in cardiac membranes. In brain and lung membranes

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the molecular weight of the "156 kDa" DAG reactive protein was ~120 kDa. The variability in molecular weight for the "156 kDa" reactive protein is maybe due to differential glycosylation of the core protein in muscle versus non-muscle tissues.

mRNA and protein expression in dystrophic muscle

RNA blot analysis of skeletal muscle mRNA from control and mdx mice of different ages using cDNA probe R43-B to 43/156 kDa mRNA revealed no reduction of 43/156 kDa DAG mRNA in mdx mice vs control mice. However, as previously observed, the 43 kDa DAG is greatly reduced in mdx skeletal muscle membranes. Thus, the absence of dystrophin causes no change in the mRNA for the 43/156 kDa DAG but leads to dramatic reductions in the amount of the 43 kDa DAG and 156 kDa DAG in skeletal muscle. Analysis of mRNA from control and DMD skeletal muscle also showed no difference in 43/156 kDa DAG mRNA expression. In agreement with findings in mdx mouse muscle, indirect immunofluorescence analysis of cryosections from normal and DMD skeletal muscle with 156 kDa specific (anti FP-D) and 43 kDa specific (anti FP-A) antibodies demonstrated a drastically reduced density of 43 kDa DAG and 156 kDa DAG in skeletal muscle of a DMD patient. Thus, 43/156 kDa DAG encoding gene is transcribed and specific mRNA is still present at the normal level in dystrophic muscle, but the 43 kDa DAG and 156 kDa DAG are greatly reduced in dystrophic muscle.

Since the 43/156 kDa DAG is expressed in non-muscle tissues we also examined expression of 43 kDa DAG in non-muscle tissues of control and mdx mice. The 156 kDa DAG could not be tested because polyclonal antibodies to the protein core of rabbit 156 kDa DAG described above do not cross react with the 156 DAG in mouse muscle.

Immunoblot analysis of brain and kidney membranes from

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control and mdx mice, stained with polyclonal anti FP-A antibodies (43 kDa specific), revealed no reduction in the amount of 43 kDa DAG in these mdx tissues. Thus, the dramatic reduction of the 43 kDa DAG that is found in mdx mice appears to be restricted to skeletal muscle and is not found in non-muscle tissues.

156 kDa DAG binds laminin

To test for the association of the 156 DAG with the extracellular matrix, rabbit skeletal muscle surface membranes and pure DGC were electrophoretically separated, transferred to the nitrocellulose membranes and overlaid with ^{125}I -labeled laminin. More specifically, rabbit skeletal muscle crude membranes, sarcolemma membranes and dystrophin-glycoprotein complex were electrophoretically separated on 3-12 % SDS polyacrylamide gels in the presence of 1% 2-mercaptoethanol and transferred to nitrocellulose. Purified laminin mouse EHS (Sigma) was iodinated with ^{125}I Na using a lactoperoxidase/glucose oxidase reaction by the Diabetes, Endocrinology Research Center at the University of Iowa. The [^{125}I]-laminin overlay procedure of Smalheiser and Schwartz (Proc. Natl. Acad. Sci. USA **84**, 6457-6461, (1987)) was performed as described except that nitrocellulose transfers were blocked with 5 % nonfat dry milk in 150 mM NaCl, 50 mM sodium phosphate, pH 7.5. To test for co-immunoprecipitation of laminin and the 156 Ka dystrophin-associated glycoprotein, pH 12 extracts (Ervasti et al., Nature **345**, 315-319 (1990)) of rabbit skeletal muscle surface membranes were incubated for 24 h at 4°C with gentle mixing buffer A (0.14 M NaCl, 1mM CaCl_2 , 1mM MgCl_2 , 10mM triethanolamine-HCl, pH 7.6) in the absence or presence of 50 μg of purified mouse EHS laminin (Sigma), then incubated for an additional 24 h at 4°C with 100 ml of either protein A-Sepharose or

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anti-laminin/ protein A-Sepharose which had been equilibrated with 3% BSA in buffer A and washed four times with buffer A. The Sepharose was pelleted by a brief centrifugation, the supernatant (void) decanted and
5 the Sepharose washed three times with buffer A.

Equivalent volumes of the resulting voids and washed Sepharose pellets were analyzed by SDS-polyacrylamide gel electrophoresis and immunoblotting using monoclonal antibody IIH6 which is specific for the 156 kDa DAG.

10 A single laminin binding band, corresponding to the 156 kDa DAG was detected in surface membranes and purified DGC. Binding of ^{125}I -laminin to the 156 DAG was significantly decreased by a 1000-fold excess of unlabeled laminin demonstrating the specificity of
15 ^{125}I -laminin binding to the 156 kDa DAG. ^{125}I -Fibronectin did not label the 156 kDa DAG or any other component of the DGC, nor did a 1000-fold excess of nonradioactive fibronectin have any effect on the binding of
20 ^{125}I -laminin to the 156 kDa DAG. The interaction of 156 kDa DAG with laminin was also shown by co-immunoprecipitation of laminin and 156 kDa DAG. Anti-laminin antibodies did not precipitate the 156 kDa DAG from alkaline extracts of rabbit skeletal muscle surface membranes. This result was consistent with the
25 observation that the surface membranes used were devoid of laminin, merosin, or S-laminin as detected on immunoblots using specific antibodies. However, anti-laminin antibodies effectively precipitated the 156 kDa DAG from alkaline extracts which had been
30 preincubated with exogenously added laminin. These results suggest that the 156 kDa DAG specifically binds laminin and may mediate interaction of DGC to extracellular matrix.

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Example 8: Human cDNA Clone

The rabbit specific insert clone R43-B (corresponding to the 156/43 coding region) was used to probe a human skeletal muscle library in λ gt10.

- 5 Screening of 10^6 clones was performed with a ^{32}P -labeled cDNA insert from R43-B rabbit clone (random primed labeling kit, Boehringer Mannheim). Hybridization was performed in 2 X Pipes, 50% deionized formamide, 0.5% SDS, 100 $\mu\text{g/ml}$ denatured salmon sperm DNA with 10^6
- 10 counts/ml of probe at 42°C overnight. Washes were done in 0.1 X SSC, 0.1% SDS at 65°C. The first human clone isolated was designated HD-1 (~2.6kb). Clones HD-2 (~3.3kb) and HD-3 (~4.1kb) were isolated from the same human library using 5' KpnI fragment from the HD-1 clone
- 15 under similar hybridization conditions.

- The chromosomal linkage of the 156 kDa and 43 kDa glycoproteins was determined by analysis of a panel of human/hamster cell hybrids (Bios, Corp.). Using a isotopically labeled cDNA insert from clone R43-B,
- 20 hybridization with human genomic DNA and hamster DNA was performed. This experiment enabled the distinction between the human and hamster genes. The same probe was then used to analyze DNA from 25 human/hamster cell hybrids which showed that the 156/43 kDa sequence was
- 25 linked to human chromosome 3.

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Example 9 Dystrophin-Associated Protein in Autosomal
Muscular Dystrophy Affected Tissue

Autosomal muscular dystrophy is a form of muscular dystrophy resulting from a mutation which maps to an autosome. It has been determined that in most cases of autosomal muscular dystrophy, dystrophin is present in affected tissue at near normal levels. This example discloses, however, that in muscle tissue from an individual afflicted with autosomal muscular dystrophy, levels of all of the dystrophin-associated proteins are substantially reduced.

Muscle biopsy tissue from an individual afflicted with autosomal Fukuyama congenital muscular dystrophy (FCMD) was prepared in sections as described, for instance, in Examples 4 and 5. The tissue samples were contacted with affinity purified sheep primary antibodies followed by fluorescein labeled secondary antibodies as described previously. Tissue samples from normal human muscle and Duchenne muscle were similarly treated as control samples.

Dystrophin and all of the dystrophin-associated glycoproteins were found to be present in normal tissue, but absent or substantially reduced in DMD muscle. However, in FCMD tissue immunostaining for all of the dystrophin-associated glycoproteins was diminished while dystrophin was not substantially reduced.

Equivalents

Those skilled in the art will recognize or be able to ascertain, using no more than routine experimentation, many equivalents to the specific embodiments of the invention described herein. Such equivalents are intended to be encompassed by the claims which follow the sequence listing.

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SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: University of Iowa Research Foundation
- (ii) TITLE OF INVENTION: DNA ENCODING DYSTROPHIN-ASSOCIATED PROTEINS
- (iii) NUMBER OF SEQUENCES: 1
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
 - (B) STREET: Two Militia Drive
 - (C) CITY: Lexington
 - (D) STATE: MA
 - (E) COUNTRY: USA
 - (F) ZIP: 02173
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 07/841,654
 - (B) FILING DATE: 20-FEB-1992
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Brook, David E.
 - (B) REGISTRATION NUMBER: 22,592
 - (C) REFERENCE/DOCKET NUMBER: UIRF89-11AA
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 617 861-6240
 - (B) TELEFAX: 617 861-9540

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4200 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

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(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 170..2855

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GGCTGCTTTT CAGGAAGATA AAGCTTTTAA GGCTGCCTAA CACTAGAAGG AGAGGCTCTC	60
GATGCTCTGG GATGGAGCAG GTGTGCAGAG GGTGAGGACC CGGCTCTGGG ATCAAGTCAC	120
TTGCTTGCTT CCTTAGCAAG ATCTTCGGCT TGAGCGAACT TGGCCTGGG ATG AGG	175
Met Arg	
1	
ATG TCT GTG GGC CTT TCA CTG CTG CTC CCC TTG TGG GGG AGG ACA TTT	223
Met Ser Val Gly Leu Ser Leu Leu Leu Pro Leu Trp Gly Arg Thr Phe	
5 10 15	
CTC CTC CTC CTC TGT GTG GCC GTG GCT CAG TCC CAT TGG CCC AGC GAA	271
Leu Leu Leu Leu Cys Val Ala Val Ala Gln Ser His Trp Pro Ser Glu	
20 25 30	
CCC TCG GAG GCT GTC AGG GAC TGG GAG AAC CAG CTG GAG GCG TCC ATG	319
Pro Ser Glu Ala Val Arg Asp Trp Glu Asn Gln Leu Glu Ala Ser Met	
35 40 45 50	
CAC TCT GTG CTC TCA GAC CTG CAC GAA GCC CTT CCC ACA GTG GTT GGC	367
His Ser Val Leu Ser Asp Leu His Glu Ala Leu Pro Thr Val Val Gly	
55 60 65	
ATT CCT GAT GGC ACG GCT GTT GTT GGG CGC TCG TTT CGA GTG ACC ATT	415
Ile Pro Asp Gly Thr Ala Val Val Gly Arg Ser Phe Arg Val Thr Ile	
70 75 80	
CCA ACA GAT TTA ATT GGC TCC AGT GGA GAA GTC ATC AAG GTA TCC ACG	463
Pro Thr Asp Leu Ile Gly Ser Ser Gly Glu Val Ile Lys Val Ser Thr	
85 90 95	
GCA GGG AAG GAG GTT TTG CCA TCG TGG CTG CAT TGG GAT CCA CAG AGC	511
Ala Gly Lys Glu Val Leu Pro Ser Trp Leu His Trp Asp Pro Gln Ser	
100 105 110	
CAC ACC CTG GAG GGC CTT CCG CTG GAC ACG GAC AAG GGT GTG CAT TAC	559
His Thr Leu Glu Gly Leu Pro Leu Asp Thr Asp Lys Gly Val His Tyr	
115 120 125 130	
ATC TCA GTG AGC GCT GCA CAG CTG GAT GCC AAC GGA AGC CAC ATC CCT	607
Ile Ser Val Ser Ala Ala Gln Leu Asp Ala Asn Gly Ser His Ile Pro	
135 140 145	
CAG ACC TCC AGT GTG TTC TCC ATC GAG GTC TAC CCC GAA GAC CAC AGT	655
Gln Thr Ser Ser Val Phe Ser Ile Glu Val Tyr Pro Glu Asp His Ser	
150 155 160	
GAG CCG CAG TCT GTG CGG GCG GCC TCT CCA GAC CTG GGC GAG GCG GCG	703
Glu Pro Gln Ser Val Arg Ala Ala Ser Pro Asp Leu Gly Glu Ala Ala	
165 170 175	
GCG TCT GCC TGT GCT GCC GAG GAG CCG GTG ACC GTC TTG ACC GTG ATT	751
Ala Ser Ala Cys Ala Ala Glu Glu Pro Val Thr Val Leu Thr Val Ile	
180 185 190	

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CTG	GAT	GCC	GAT	CTC	ACC	AAG	ATG	ACT	CCG	AAG	CAG	AGG	ATC	GAC	CTC	799
Leu	Asp	Ala	Asp	Leu	Thr	Lys	Met	Thr	Pro	Lys	Gln	Arg	Ile	Asp	Leu	
195					200					205					210	
CTG	CAC	AGG	ATG	CAG	AGC	TTC	TCG	GAG	GTG	GAG	CTC	CAC	AAC	ATG	AAG	847
Leu	His	Arg	Met	Gln	Ser	Phe	Ser	Glu	Val	Glu	Leu	His	Asn	Met	Lys	
				215				220						225		
TTG	GTG	CCG	GTG	GTG	AAT	AAC	AGA	CTG	TTT	GAT	ATG	TCT	GCC	TTC	ATG	895
Leu	Val	Pro	Val	Val	Asn	Asn	Arg	Leu	Phe	Asp	Met	Ser	Ala	Phe	Met	
			230					235					240			
GCC	GGC	CCC	GGA	AAC	GCC	AAA	AAG	GTG	GTA	GAG	AAC	GGG	GCC	CTG	CTC	943
Ala	Gly	Pro	Gly	Asn	Ala	Lys	Lys	Val	Val	Glu	Asn	Gly	Ala	Leu	Leu	
		245					250					255				
TCC	TGG	AAG	CTG	GGC	TGC	TCC	CTG	AAC	CAG	AAC	AGT	GTG	CCT	GAC	ATT	991
Ser	Trp	Lys	Leu	Gly	Cys	Ser	Leu	Asn	Gln	Asn	Ser	Val	Pro	Asp	Ile	
	260					265					270					
CGC	GGC	GTG	GAG	GCC	CCT	GCC	AGG	GAG	GGC	ACT	ATG	TCT	GCC	CAG	CTT	1039
Arg	Gly	Val	Glu	Ala	Pro	Ala	Arg	Glu	Gly	Thr	Met	Ser	Ala	Gln	Leu	
275					280					285					290	
GGC	TAC	CCT	GTG	GTG	GGT	TGG	CAC	ATT	GCC	AAC	AAG	AAG	CCA	CCT	CTC	1087
Gly	Tyr	Pro	Val	Val	Gly	Trp	His	Ile	Ala	Asn	Lys	Lys	Pro	Pro	Leu	
			295						300					305		
CCC	AAG	CGT	ATC	CGA	AGG	CAG	ATC	CAT	GCC	ACA	CCC	ACA	CCT	GTC	ACT	1135
Pro	Lys	Arg	Ile	Arg	Arg	Gln	Ile	His	Ala	Thr	Pro	Thr	Pro	Val	Thr	
			310					315					320			
GCC	ATT	GGG	CCC	CCA	ACC	ACG	GCC	ATC	CAG	GAG	CCG	CCG	TCC	AGG	ATC	1183
Ala	Ile	Gly	Pro	Pro	Thr	Thr	Ala	Ile	Gln	Glu	Pro	Pro	Ser	Arg	Ile	
		325					330					335				
GTG	CCT	ACC	CCC	ACT	TCT	CCA	GCC	ATT	GCT	CCT	CCC	ACA	GAG	ACG	ATG	1231
Val	Pro	Thr	Pro	Thr	Ser	Pro	Ala	Ile	Ala	Pro	Pro	Thr	Glu	Thr	Met	
	340					345					350					
GCT	CCT	CCA	GTC	AGG	GAT	CCT	GTT	CCT	GGG	AAG	CCC	ACG	GTC	ACC	ACT	1279
Ala	Pro	Pro	Val	Arg	Asp	Pro	Val	Pro	Gly	Lys	Pro	Thr	Val	Thr	Thr	
355					360					365					370	
CGG	ACT	CGA	GGT	GCC	ATT	ATT	CAG	ACC	CCA	ACC	CTA	GGC	CCC	ATC	CAG	1327
Arg	Thr	Arg	Gly	Ala	Ile	Ile	Gln	Thr	Pro	Thr	Leu	Gly	Pro	Ile	Gln	
			375						380					385		
CCC	ACT	CGG	GTG	TCA	GAC	GCT	GGC	ACC	GTA	GTT	TCT	GGC	CAG	ATT	CGT	1375
Pro	Thr	Arg	Val	Ser	Asp	Ala	Gly	Thr	Val	Val	Ser	Gly	Gln	Ile	Arg	
			390					395					400			
GCA	ACG	GTG	ACC	ATT	CCT	GGC	TAC	GTG	GAG	CCC	ACA	GCA	GTT	GCC	ACC	1423
Ala	Thr	Val	Thr	Ile	Pro	Gly	Tyr	Val	Glu	Pro	Thr	Ala	Val	Ala	Thr	
		405					410					415				
CCT	CCC	ACA	ACT	ACA	ACC	AAA	AAG	CCA	CGA	GTG	TCC	ACA	CCA	AAA	CCA	1471
Pro	Pro	Thr	Thr	Thr	Thr	Lys	Lys	Pro	Arg	Val	Ser	Thr	Pro	Lys	Pro	
	420					425					430					

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GCA Ala 435	ACG Thr	CCT Pro	TCA Ser	ACG Thr	GAC Asp 440	TCC Ser	TCA Ser	GCC Ala	ACC Thr	ACG Thr 445	ACT Thr	CGC Arg	AGG Arg	CCA Pro	ACC Thr 450	1519
AAG Lys	AAG Lys	CCA Pro	CGG Arg	ACA Thr 455	CCC Pro	AGG Arg	CCG Pro	GTG Val	CCA Pro 460	CGG Arg	GTC Val	ACC Thr	ACT Thr	AAA Lys 465	GCT Ala	1567
CCC Pro	ATC Ile	ACC Thr	AGG Arg 470	CTG Leu	GAG Glu	ACG Thr	GCC Ala	TCC Ser 475	CCA Pro	CCT Pro	ACT Thr	CGT Arg	ATC Ile 480	CGC Arg	ACC Thr	1615
ACC Thr	ACC Thr	AGC Ser 485	GGG Gly	GTG Val	CCC Pro	CGC Arg	GGG Gly 490	GGA Gly	GAA Glu	CCC Pro	AAC Asn	CAG Gln 495	CGC Arg	CCA Pro	GAG Glu	1663
CTC Leu	AAG Lys 500	AAC Asn	CAC His	ATC Ile	GAC Asp 505	AGG Arg	GTG Val	GAC Asp	GCC Ala	TGG Trp 510	GTC Val	GGC Gly	ACC Thr	TAC Tyr	TTT Phe	1711
GAG Glu 515	GTG Val	AAG Lys	ATC Ile	CCA Pro	TCT Ser 520	GAT Asp	ACC Thr	TTC Phe	TAC Tyr	GAC Asp 525	AAG Lys	GAG Glu	GAT Asp	ACC Thr	ACC Thr 530	1759
ACC Thr	GAC Asp	AAG Lys	CTC Leu 535	AAG Lys	CTG Leu	ACC Thr	CTG Leu	AAG Lys	CTG Leu 540	CGA Arg	GAG Glu	CAG Gln	CAG Gln	CTG Leu 545	GTG Val	1807
GGC Gly	GAG Glu	AAG Lys 550	TCC Ser	TGG Trp	GTG Val	CAG Gln	TTC Phe	AAC Asn 555	AGC Ser	AAC Asn	AGC Ser	CAG Gln	CTC Leu 560	ATG Met	TAT Tyr	1855
GGC Gly	CTG Leu	CCC Pro 565	GAC Asp	AGC Ser	AGC Ser	CAC His	GTG Val 570	GGC Gly	AAA Lys	CAC His	GAG Glu	TAT Tyr 575	TTC Phe	ATG Met	CAT His	1903
GCC Ala 580	ACA Thr	GAC Asp	AAG Lys	GGA Gly	GCC Gly	CTG Leu 585	TCC Ser	GCC Ala	GTG Val	GAT Asp	GCC Ala 590	TTT Phe	GAG Glu	ATC Ile	CAT His	1951
GTC Val 595	CAC His	AAG Lys	CGC Arg	CCT Pro	CAA Gln 600	GGG Gly	GAC Asp	AAA Lys	GCT Ala	CCT Pro 605	GCT Ala	CGT Arg	TTC Phe	AAA Lys	GCC Ala 610	1999
AAG Lys	TTC Phe	GTG Val	GGT Gly	GAC Asp 615	CCA Pro	GCG Ala	CCA Pro	GTG Val	GTG Val	AAT Asn 620	GAC Asp	ATC Ile	CAC His	AAG Lys 625	AAG Lys	2047
ATT Ile	GCC Ala	CTG Leu 630	GTG Val	AAG Lys	AAG Lys	CTG Leu	GCC Ala	TTT Phe 635	GCC Ala	TTT Phe	GGG Gly	GAT Asp	CGC Arg	AAT Asn 640	TGC Cys	2095
AGC Ser	ACC Thr	GTC Val 645	ACC Thr	CTG Leu	CAG Gln	AAC Asn	ATC Ile 650	ACC Thr	CGC Arg	GGC Gly	TCC Ser	ATT Ile 655	GTG Val	GTG Val	GAG Glu	2143
TGG Trp 660	ACC Thr	AAC Asn	AAC Asn	ACA Thr	CTG Leu	CCG Pro 665	CTG Leu	GAG Glu	CCC Pro	TGC Cys	CCC Pro	AAG Lys	GAG Glu	CAG Gln	ATC Ile	2191

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ACG	GCG	CTG	AGC	GGC	AGG	ATC	GCC	GAG	GAC	AAC	GGG	CAG	CCT	CGG	CCA
Thr	Gly	Leu	Ser	Arg	Arg	Ile	Ala	Glu	Asp	Asn	Gly	Gln	Pro	Arg	Pro
675				680						685					690
GCC	TTC	ACC	AAT	GCC	CTG	GAG	CCT	GAC	TTT	AAG	GCC	ACG	AGC	ATC	GCC
Ala	Phe	Thr	Asn	Ala	Leu	Glu	Pro	Asp	Phe	Lys	Ala	Thr	Ser	Ile	Ala
				695					700					705	
ATA	ACG	GGC	TCT	GGC	AGT	TGT	CGG	CAC	TTG	CAG	TTT	ATC	CCC	GTG	GCA
Ile	Thr	Gly	Ser	Gly	Ser	Cys	Arg	His	Leu	Gln	Phe	Ile	Pro	Val	Ala
			710					715					720		
CCG	CCT	GGG	ATC	CCG	TCC	TCG	GTG	ACA	CCA	CCC	ACG	GAG	GTG	CCA	GAC
Pro	Pro	Gly	Ile	Pro	Ser	Ser	Val	Thr	Pro	Pro	Thr	Glu	Val	Pro	Asp
		725					730					735			
AGG	GAC	CCC	GAG	AAG	AGC	AGT	GAG	GAT	GAC	GTC	TAC	CTA	CAC	ACA	GTC
Arg	Asp	Pro	Glu	Lys	Ser	Ser	Glu	Asp	Asp	Val	Tyr	Leu	His	Thr	Val
	740					745					750				
ATT	CCG	GCT	GTG	GTG	GTG	GCG	GCC	ATC	CTG	CTC	ATT	GCT	GGC	ATC	ATT
Ile	Pro	Ala	Val	Val	Val	Ala	Ala	Ile	Leu	Leu	Ile	Ala	Gly	Ile	Ile
755				760						765					770
GCC	ATG	ATC	TGC	TAC	CGC	AAG	AAG	CGG	AAG	GGC	AAG	CTC	ACC	CTG	GAG
Ala	Met	Ile	Cys	Tyr	Arg	Lys	Lys	Arg	Lys	Gly	Lys	Leu	Thr	Leu	Glu
				775					780					785	
GAC	CAG	GCC	ACC	TTC	ATC	AAG	AAG	GGG	GTG	CCC	ATC	ATC	TTT	GCA	GAC
Asp	Gln	Ala	Thr	Phe	Ile	Lys	Lys	Gly	Val	Pro	Ile	Ile	Phe	Ala	Asp
			790					795					800		
GAG	CTG	GAC	GAC	TCC	AAG	CCC	CCG	CCC	TCC	TCC	AGC	ATG	CCG	CTG	ATC
Glu	Leu	Asp	Asp	Ser	Lys	Pro	Pro	Pro	Ser	Ser	Ser	Met	Pro	Leu	Ile
		805					810					815			
CTG	CAG	GAG	GAG	AAG	GCT	CCC	CTT	CCC	CCC	CCA	GAG	TAT	CCC	AGC	CAG
Leu	Gln	Glu	Glu	Lys	Ala	Pro	Leu	Pro	Pro	Pro	Glu	Tyr	Pro	Ser	Gln
	820					825					830				
AGC	GTG	CCC	GAG	ACC	ACG	CCT	CTG	AAC	CAG	GAC	ACT	GTG	GGG	GAG	TAC
Ser	Val	Pro	Glu	Thr	Thr	Pro	Leu	Asn	Gln	Asp	Thr	Val	Gly	Glu	Tyr
835					840					845					850
ACG	CCC	CTT	CGG	GAT	GAG	GAT	CCC	AAC	GCG	CCT	CCC	TAC	CAG	CCC	CCC
Thr	Pro	Leu	Arg	Asp	Glu	Asp	Pro	Asn	Ala	Pro	Pro	Tyr	Gln	Pro	Pro
				855				860						865	
CCA	CCC	TTC	ACA	GCC	CCG	ATG	GAG	GGC	AAG	GGC	TCC	CGT	CCC	AAG	AAC
Pro	Pro	Phe	Thr	Ala	Pro	Met	Glu	Gly	Lys	Gly	Ser	Arg	Pro	Lys	Asn
			870					875					880		
ATG	ACC	CCT	TAC	CGG	TCA	CCC	CCT	CCT	TAT	GTT	CCC	CCT	T	AACCCACAAG	
Met	Thr	Pro	Tyr	Arg	Ser	Pro	Pro	Pro	Tyr	Val	Pro	Pro			
		885					890					895			

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GACTTTGGGG	ACTTTTTTTA	TTTTATTTT	TTGCCTAACA	GCTTTTGT	TGTTTCATAGA	3105
AAATCCTTCG	CTGCGTTTTG	ATGGCTGGCT	CTGGAAGCAC	CATTTGGAGT	AGAGGTAGAG	3165
GGAGGGAGCG	AGGAGCOGTG	GGTGAACG	CAGGCAGTGC	TGGGCAGCCC	CCCGGCTCTC	3225
TGCGTTTTGC	CTTTAACT	AACGTACTG	TTTTTCTAT	TCACGTGTGT	CTAGCTGCAG	3285
GATGTAACAT	GGAAAACAGT	AGCTAAAGAT	TAAATTCAAA	GGACTTTCAG	AAGTTAAGGT	3345
TAAGTTTTTA	CATTTAATCT	GCTGTTTACC	TAACTTGTA	TGTATAATT	TTGGGTGGGT	3405
ATGGGGAATT	GCTTGCTAA	AAATAAGCTC	CCAGGTGT	TCAAACCTAA	GAGAAGACCA	3465
AGGGACAGTA	TTTTTATCA	AAGGAATCCT	ATTTTTTCAC	ACTATGTCAA	CTTGGTTGCT	3525
CTGATATCCC	AGAGCCCGAT	CGGGGGCCTC	CTGGCCCTGG	CTCAGGGGCC	AGGGTCCTGG	3585
TGCTGGGTTT	GCTCTCCTGC	TGTTGGCAGG	AGTTGGAAGC	TGGAGGGGCC	TCTCGGGCCG	3645
TGGACATCCC	CACCTCCACC	CCATGCATGC	TAGTGGCCCA	CCACCAAGGG	GTCTTCATTT	3705
CCATGGGAAA	GGGACTCCAA	GAGGCAGTGG	TGGCCGTGGC	CCCCACCCCG	GGTGCTCCAA	3765
GGTGGGCCAG	CTGCTCGTGG	GGGCCCCCTG	GGAGGTGAG	GGACTCGACC	ACATCGACCT	3825
GTTTCCTTTC	ACCTTTTATT	TTTTTTTTTC	CCCACCCCTC	CTAAAAGGAT	TATCACGGTT	3885
TTTGAAACAC	TCAGTGGGGG	ACATTTTGGT	GAAGATGCAA	TATTTTTATG	TCATGTGATG	3945
CTCTTTCCTC	ACTTGACCTT	GGCCACTTTG	TCCCAACAGT	CCACAGCCCC	GCCCCGATCC	4005
ACCCCATCCC	TCTTCTCTGG	CGCTCCCGTC	CCAGGCCTTG	GGCCTGAACG	ACTGGAAAAG	4065
GCCTGGTTGG	CTGGGGAGGA	GTGCCACCAA	TAGTTCATAG	TAAACAATCT	GTGGGCTCTC	4125
AAAGCTAATT	TTTACTAAA	GTTTTTATAC	AGCCTCAAAT	TGTTTTATTA	AAAAATAGAT	4185
TAAAAATGGT	GATGC					4200

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CLAIMS

1. A substantially pure nucleic acid sequence encoding at least a portion of the 43 kDa non-dystrophin component of the dystrophin-glycoprotein complex.
2. A substantially pure nucleic acid sequence of Claim 1 which is of human origin.
3. A substantially pure nucleic acid sequence of Claim 2 which is characterized by the ability to hybridize to the DNA sequence of SEQ ID NO: 1, or the complement thereof, under stringent hybridization conditions.
4. A substantially pure nucleic acid sequence encoding at least a portion of the 156 kDa non-dystrophin component of the dystrophin-glycoprotein complex.
5. A substantially pure nucleic acid sequence of Claim 4 which is of human origin.
6. A substantially pure nucleic acid sequence of Claim 5 which is characterized by the ability to hybridize to the DNA sequence of SEQ ID NO: 1, or the complement thereof, under stringent hybridization conditions.
7. A DNA expression construct comprising, in expressible form, a substantially pure deoxyribonucleic acid sequence encoding at least a portion of the 43 kDa non-dystrophin component of the dystrophin-glycoprotein complex.

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8. A DNA expression construct of Claim 7 which is of human origin.
9. A DNA expression construct of Claim 8 which is characterized by the ability to hybridize to the DNA sequence of SEQ ID NO: 1, or the complement thereof, under stringent hybridization conditions.
10. A DNA expression construct comprising, in expressible form, a substantially pure deoxyribonucleic acid sequence encoding at least a portion of the 156 kDa non-dystrophin component of the dystrophin-glycoprotein complex.
11. A DNA expression construct of Claim 10 which is of human origin.
12. A DNA expression construct of Claim 11 which is characterized by the ability to hybridize to the DNA sequence of SEQ ID NO: 1, or the complement thereof, under stringent hybridization conditions.
13. A prokaryotic cell transformed with a DNA expression construct comprising, in expressible form, a substantially pure deoxyribonucleic acid sequence encoding at least a portion of the 43 kDa non-dystrophin component of the dystrophin-glycoprotein complex.
14. A prokaryotic cell of Claim 13 wherein the substantially pure deoxyribonucleic acid sequence is characterized by the ability to hybridize to the DNA sequence of SEQ ID NO: 1, or the complement thereof, under stringent hybridization conditions.

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15. A prokaryotic cell transformed with a DNA expression construct comprising, in expressible form, a substantially pure deoxyribonucleic acid sequence encoding at least a portion of the 156 kDa non-dystrophin component of the dystrophin-glycoprotein complex.
16. A prokaryotic cell of Claim 15 wherein the substantially pure deoxyribonucleic acid sequence is characterized by the ability to hybridize to the DNA sequence of SEQ ID NO: 1, or the complement thereof, under stringent hybridization conditions.
17. A eukaryotic cell transformed with a DNA expression construct comprising, in expressible form, a substantially pure deoxyribonucleic acid sequence encoding at least a portion of the 43 kDa non-dystrophin component of the dystrophin-glycoprotein complex.
18. A eukaryotic cell of Claim 17 wherein the substantially pure deoxyribonucleic acid sequence is characterized by the ability to hybridize to the DNA sequence of SEQ ID NO: 1, or the complement thereof, under stringent hybridization conditions.
19. A eukaryotic cell transformed with a DNA expression construct comprising, in expressible form, a substantially pure deoxyribonucleic acid sequence encoding at least a portion of the 156 kDa non-dystrophin component of the dystrophin-glycoprotein complex.

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20. A eukaryotic cell of Claim 19 wherein the substantially pure deoxyribonucleic acid sequence is characterized by the ability to hybridize to the DNA sequence of SEQ ID NO: 1, or the complement thereof, under stringent hybridization conditions.
21. A method for producing a substantially pure preparation of at least a portion of the 43 kDa component of the dystrophin-glycoprotein complex, comprising the steps of:
 - a) providing a cell harboring a DNA expression construct comprising, in expressible form, a substantially pure deoxyribonucleic acid sequence encoding at least a portion of the 43 kDa non-dystrophin component of the dystrophin-glycoprotein complex; and
 - b) isolating the product encoded by the expression construct from the cell.
22. A method for producing a substantially pure preparation of at least a portion of the 156 kDa component of the dystrophin-glycoprotein complex, comprising the steps of:
 - a) providing a cell harboring a DNA expression construct comprising, in expressible form, a substantially pure deoxyribonucleic acid sequence encoding at least a portion of the 156 kDa non-dystrophin component of the dystrophin-glycoprotein complex; and
 - b) isolating the product encoded by the expression construct from the cell.